

STIC-Biotech/ChemLib

85030

From: Sullivan, Daniel
Sent: Thursday, January 23, 2003 12:39 PM
To: STIC-Biotech/ChemLib
Subject: SEQUENCE SEARCH FOR 09852424

Please search for a polypeptide comprising the sequence set forth as SEQ ID NO:1-5 in the commercial and issued patent databases.

Thank you.
Dan

Daniel M. Sullivan
Examiner AU 1636
Room: 12D12
Mail Box: 11E12
Tel: 703-305-4448

RECEIVED

JAN 23 2003

STIC/BIOTECH DIVISION
(STIC)

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

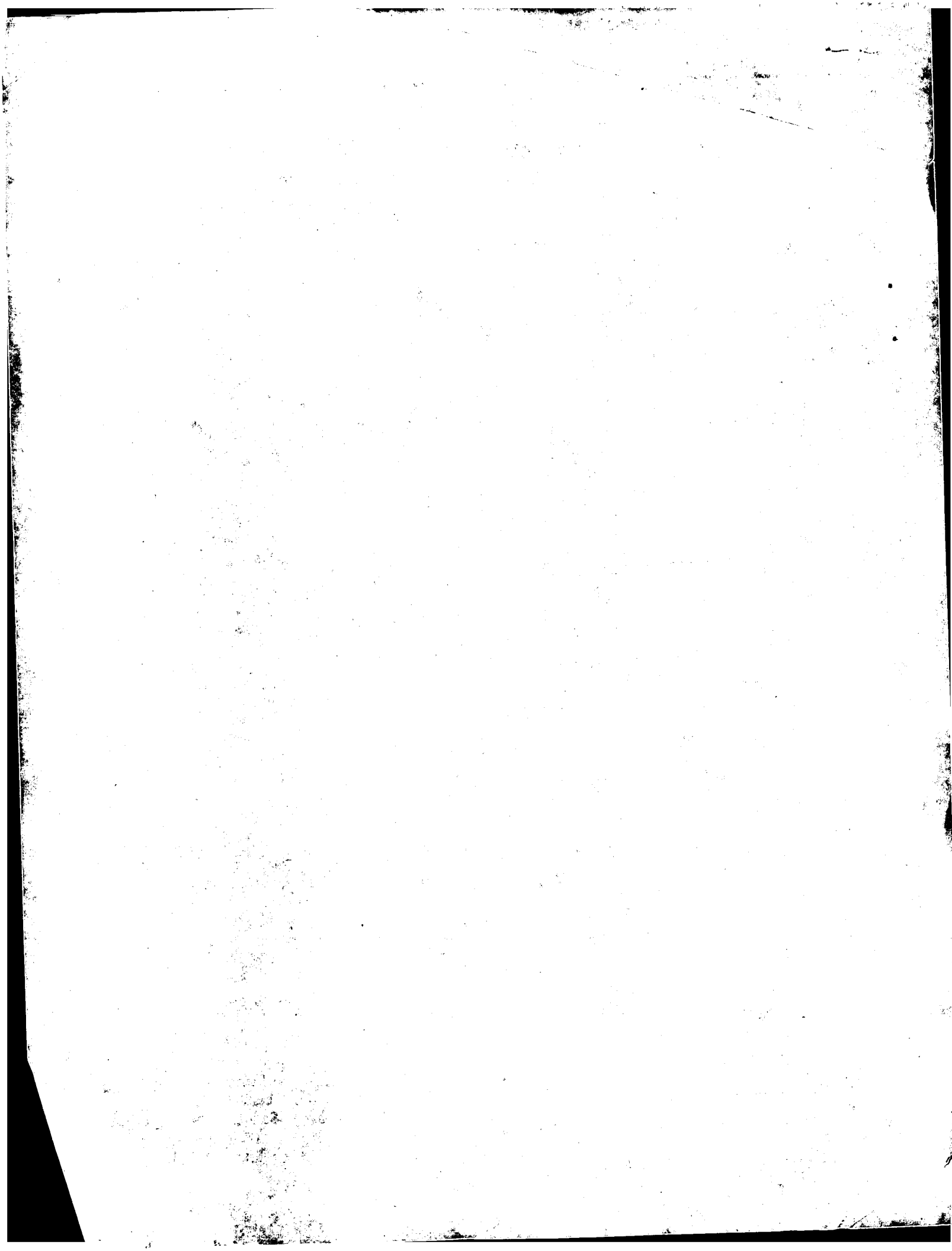
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/23/03
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 5
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:27:48 ; Search time 28.2 seconds
(without alignments)
316.588 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359
Sequence: 1 KGVSLSYRCPCRFESHVAR.....QVCIDPKLKIQIYLEKALN 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	67	23	AA48656
2	354	98.6	67	23	AA48658
3	352	98.1	67	23	AA48657
4	352	98.1	67	23	AA48660
5	351	97.8	67	19	AA50760
6	351	97.8	67	20	AA534092
7	351	97.8	67	20	AA506741
8	351	97.8	67	20	AA506726
9	351	97.8	67	21	AA567594
10	351	97.8	67	23	AA847660

11	351	97.8	68	19	AA50761	Peptide which bind
12	351	97.8	69	20	AA50818	N-terminal modifie
13	351	97.8	72	19	AA50762	Peptide which bind
14	351	97.8	72	20	AA534092	Native stromal cel
15	351	97.8	73	21	AA567595	SDF-1beta peptide
16	351	97.8	73	19	AA50763	Peptide which bind
17	351	97.8	73	20	AA505819	N-terminal modifie
18	351	97.8	74	21	AA569041	Amino acid sequenc
19	351	97.8	89	16	AA575419	Human SDF-1-alpha.
20	351	97.8	89	20	AA539995	Human SDF-1 deriv
21	351	97.8	89	20	AA526177	Human chemokine SD
22	351	97.8	89	21	AA515791	A human B-cell stl
23	351	97.8	89	21	AA593603	N-terminal modifie
24	351	97.8	89	21	AA552508	Human SDF-1-which
25	351	97.8	90	20	AA505820	Stromal cell deriv
26	351	97.8	93	16	AA575420	Amino acid sequenc
27	351	97.8	93	19	AA50766	Human chemokine SD
28	351	97.8	93	20	AA526178	Human stromal cell
29	351	97.8	93	20	AA506725	Human SDF-1-precu
30	351	97.8	93	21	AA515812	SDF-1-beta. Homo
31	351	97.8	93	23	AA523952	N-terminal modifie
32	351	97.8	93	23	AA5084305	SDF-1gamma SEQ ID
33	351	97.8	93	23	AA547690	Human SDF-1 beta a
34	351	97.8	93	20	AA505821	Human SDF-1 beta a
35	351	97.8	101	23	AA48047	Human SDF-1 beta a
36	351	97.8	119	23	AA48047	Human SDF-1 beta a
37	351	97.8	166	20	AA529899	Human SDF-1 beta a
38	351	97.8	177	20	AA529896	A chemokine recept
39	351	97.8	320	21	AA569055	A chemokine recept
40	351	97.8	322	21	AA569056	Human chemokine SD
41	351	97.8	326	19	AA567521	A chemokine recept
42	351	97.8	327	21	AA569057	Human chemokine SD
43	351	97.8	328	19	AA567522	Human chemokine SD
44	351	97.8	328	19	AA567522	Human SDF-1 and hu
45	351	97.8	339	20	AA529905	

ALIGNMENTS

RESULT 1
AA48656
AA48656 standard; peptide: 67 AA.

AC AA48656;
20-MAY-2002 (first entry)

DT XX
DT XX
DT XX
DE CXCR4 peptide antagonist SEQ ID NO 1.

XX CXCR4; haematopoietic cell; chemokine receptor-4; cytosolic;
KW Immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW cell multiplication.
KW
KW
XX
XX
OS Synthetic.
XX
XX WO200185196-A2.
PN
PD 15-NOV-2001.
PD
PF 09-MAY-2001; 2001WO-CA00659.
PF
XX 09-MAY-2000; 2000CA-2305787.
XX 19-MAY-2000; 2000US-205467P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI Clark-Lewis I, Salari H;
XX WPI: 2002-106073/14.
DR
XX

PT Promoting the rate of haematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the
 PT cells
 PS Claim 9, Page 54; 68pp; English.

CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 SQ Sequence 67 AA:

Query Match 100.0%; Score 359; DB 23; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 DB 1 KGVSLSYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 2

AAM48658
 ID AAM48658 standard; peptide; 67 AA.

AC AAM48658;

DT 20-MAY-2002 (first entry)

DE CXCR4 peptide antagonist SEQ ID NO 3.

KW CRX4; haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.

OS Synthetic.

Key Location/Qualifiers
 Modified-site 6

FT /note= "Optionally the proline analogue 6-amino-7-oxo-2,
 FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
 FT acid residue or a bicyclic turned dipeptide
 FT (Btd)"

W0200185196-A2.

15-NOV-2001.

09-MAY-2001; 2001WO-CA00659.

09-MAY-2000; 2000CA-2305787.

19-MAY-2000; 2000US-205467P.

(UYBR-) UNIV BRITISH COLUMBIA.

(CHEM-) CHEMOKINE THERAPEUTICS CORP.

Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;

WPI; 2002-106073/14.

PT Promoting the rate of haematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the
 PT cells
 PS Claim 9, Page 54; 68pp; English.

CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 SQ Sequence 67 AA:

Query Match 98.6%; Score 354; DB 23; Length 67;
 Best Local Similarity 98.5%; Pred. No. 5.5e-39;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 DB 1 KGVSLPYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 3

AAM48657
 ID AAM48657 standard; peptide; 67 AA.

AC AAM48657;

DT 20-MAY-2002 (first entry)

DE CXCR4 peptide antagonist SEQ ID NO 2.

KW CRX4; haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.

OS Synthetic.

Key Location/Qualifiers
 Modified-site 5

FT /note= "Optionally the proline analogue 6-amino-7-oxo-2,
 FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
 FT acid residue or a bicyclic turned dipeptide
 FT (Btd)"

W0200185196-A2.

15-NOV-2001.

09-MAY-2001; 2001WO-CA00659.

09-MAY-2000; 2000CA-2305787.

19-MAY-2000; 2000US-205467P.

(UYBR-) UNIV BRITISH COLUMBIA.

(CHEM-) CHEMOKINE THERAPEUTICS CORP.

Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;

WPI; 2002-106073/14.

CC associated opportunistic infections and/or other CXC or CC chemokines,
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.

XX
 SQ Sequence 67 AA:

Query Match 97.8%; Score 351; DB 19; Length 67;
 Best Local Similarity 98.5%; Pred. No. 1.4e-38;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVKKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANVKKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 6
 AAY34092
 ID AAY34092 standard; protein: 67 AA.

XX AAY34092;
 XX
 DT 29-NOV-1999 (first entry)

XX Native stromal cell derived factor 1 (SDF-1) alpha protein.

KW CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KM interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KM angiogenesis; stromal cell derived factor 1; SDF-1.

XX Mammalia.

XX WO9947158-A2.

XX 23-SEP-1999.

XX 12-MAR-1999; 99WO-CA00221.

XX 13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Duronio V;

PI WPI; 1999-561857/47.

XX Use of CXC chemokine receptor 4 for treating autoimmune disease and
 PT cancer -

XX Example 1; Fig 1; 71pp: English.

XX The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)
 CC antagonist for the manufacture of a medicament for reducing interferon
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
 CC to treat or to design a medicament to treat, an autoimmune disease,
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
 CC antagonists may be peptide compounds comprising a substantially purified
 CC peptide fragment, analogue or a pharmacologically acceptable salt of
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents
 CC the amino acid sequence of SDF-1 alpha protein.

XX Sequence 67 AA:

Query Match 97.8%; Score 351; DB 20; Length 67;
 Best Local Similarity 98.5%; Pred. No. 1.4e-38;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVKKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANVKKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 7
 AAY06741
 ID AAY06741 standard; protein: 67 AA.

XX AAY06741;

DT 18-JUN-1999 (first entry)

XX SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

KW Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
 KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV;
 KM stromal cell derived factor 1; Macrophage Inflammatory protein.

XX Synthetic.

XX Homo sapiens.

XX WO9911655-A1.

XX 11-MAR-1999.

XX 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCT.

XX Kent SBH, Siani MA, Simon R, Wilken J;

DR WPI; 1999-205128/17.

XX New cross-over proteins for treatment of inflammation and infections
 PT e.g. AIDS - prepared by ligation of two functional protein modules
 PT derived from two different parent molecules

XX Example 4; Page 43; 75pp: English.

XX The invention relates to a cross-over protein produced by chemical
 CC ligation of at least two functional protein modules derived from at
 CC least two parent protein molecules. The cross-over proteins can be used
 CC in pharmaceutical compositions for therapy of inflammatory and
 CC infectious diseases including AIDS, and for indications of hematopoiesis
 CC and chemoprotection. They are also useful for treatment of asthma,
 CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library
 CC comprising a collection of cross-over proteins is useful for screening
 CC for cross-over proteins that are receptor ligands. The libraries
 CC comprise functionally diverse compounds and libraries are exemplified by the
 CC discovery process. The proteins and libraries are exemplified by the
 CC preparation of cross-over chemokines comprising various combinations of
 CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor
 CC 1), VMP (viral Macrophage Inflammatory protein) and other such
 CC chemokines. Sequences AAY06741-62 represent amino acid sequences of SDF-1
 CC alpha/RANTES cross-over molecules.

XX Sequence 67 AA:

Query Match 97.8%; Score 351; DB 20; Length 67;
 Best Local Similarity 98.5%; Pred. No. 1.4e-38;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVKKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANVKKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 8

ID AAY06726 standard; protein; 67 AA.

AC AAY06726;

DT 18-JUN-1999 (first entry)

DE Amino acid fragment of SDF-1 alpha.

KM Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;
KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;
KM stromal cell derived factor 1; Macrophage inflammatory protein.

OS Homo sapiens.

OS Synthetic.

PN WO911655-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

PA (GRYP-) GRYPHON SCI.

PI Kent SBH, Stanl MA, Simon R, Wilken J;

DR WPI; 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections
PT e.g. AIDS - prepared by ligation of two functional protein modules
PT derived from two different parent molecules

PS Example 4; Page 41; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical
CC ligation of at least two functional protein modules derived from at least
CC two parent protein molecules. The cross-over proteins can be used in
CC pharmaceutical compositions for therapy of inflammatory and infectious
CC diseases including AIDS, and for indications of hematopoiesis and
CC chemoprotection. They are also useful for treatment of asthma, allergic
CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library
CC comprising a collection of cross-over proteins is useful for screening
CC for cross-over proteins that are receptor ligands. The libraries comprise
CC functionally diverse compounds therefore improving the drug discovery
CC process. The proteins and libraries are exemplified by the preparation
CC of cross-over chemokines comprising various combinations of peptide
CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMP
CC (viral Macrophage inflammatory protein) and other such chemokines. The
CC present sequence represents an amino acid fragment of SDF-1 alpha which
CC acts as a synthetic base molecule for synthesizing the cross-over
CC protein.

SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 20; Length 67;
Best Local Similarity 98.5%; Pred. No. 1.4e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQVSLSYRCPCRFESHVARANKYHLKILNTPCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KQVSLSYRCPCRFESHVARANKYHLKILNTPCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67

DB 61 YLEKALN 67

RESULT 9

ID AAY67594 standard; peptide; 67 AA.

AC AAY67594;

DT 13-JUN-2000 (first entry)

DE SDF-1alpha peptide sequence.

KM SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
KM autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KM type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;
KM stromal cell derived factor one; anti-inflammatory; immunomodulatory.

OS Unidentified.

PN WO200009152-A1.

PD 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI; 2000-224175/19.

PT Therapeutic composition containing CXCR4 antagonist, useful for
PT treating autoimmune disease, especially multiple sclerosis and cancer
PT -

PS Disclosure: Fig 1; 88pp; English.

CC The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells, particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1alpha
CC peptide sequence.

SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 21; Length 67;
Best Local Similarity 98.5%; Pred. No. 1.4e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQVSLSYRCPCRFESHVARANKYHLKILNTPCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KQVSLSYRCPCRFESHVARANKYHLKILNTPCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 10
AAB47680

ID	AA847680 standard; peptide: 67 AA.
XX	
AC	AA847680:
XX	
DT	30-JAN-2002 (first entry)
XX	
DE	SDF-1-alpha.
XX	
KM	Hematopoietic cell; multiplication: CXK chemokine receptor 4; CXCR4;
KW	agonist; Stromal cell derived factor one; SDF-1; autoimmune disease;
KW	macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KX	autologous; allogenic; bone marrow; stem cell; transplantation.
OS	
XX	Homo sapiens.
PX	
PN	MO200176615-A2.
PD	
PD	18-OCT-2001.
PF	
XX	12-APR-2001; 2001WO-CO0540.
PR	
PR	12-APR-2000; 2000CA-2305036.
PR	14-SEP-2000; 2000US-232425P.
XX	23-FEB-2001; 2001CA-2335109.
PA	(UYBR-) UNITV BRITISH COLUMBIA.
PI	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI	Cashman J, Clark-Lewis I;
DR	WPI: 2002-025882/03.
XX	
PT	CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT	and susceptibility to cytotoxic agents, are useful for bone marrow or
PT	peripheral blood stem cell transplantation -
PS	Claim 8; Page 57; 74pp; English.
XX	
CC	The sequences given in AA847680-717 represent peptides which may be
CC	used in the method of the invention for reducing the rate of
CC	hematopoietic cell multiplication. These peptides act as CXK chemokine
CC	receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC	stromal cell derived factor one (SDF-1) with some also containing
CC	sequences derived from macrophage inflammatory protein 1-alpha
CC	(MIP-1-alpha). They can be used to reduce susceptibility of
CC	hematopoietic cells to a cytotoxic agent, by administering one of the
CC	agonist peptides to the cells prior to or during exposure of the
CC	cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC	susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC	in a patient with cancer requiring autologous or allogeneic bone marrow
CC	or peripheral blood stem cell transplantation, or an autoimmune disease.
XX	
SQ	Sequence 67 AA:
Query Match	97.8%; Score 351; DB 23; Length 67;
Best Local Similarity	98.5%; Pred. No. 1.4e-38;
Matches 66; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	I KGVSLSYRCPCRFPPESHVARAVWKHLKLINTFNCALQIVARLKNNNROYCIPKTKIOE 60 I Db 1 KPVSLSYRCPCRFPPESHVARAVWKHLKLINTFNCALQIVARLKNNNROYCIPKTKIOE 60
OY	61 YLEKALN 67 Db 61 YLEKALN 67
RESULT 11	
AAW50761	
ID	AAW50761 standard; peptide: 68 AA.
XX	
CC	AAW50761;

XX	DT	27-JUL-1998	(first entry)	
XX	XX	Peptide which binds to CXCR4 receptor and is useful for treating HIV.		
XX	XX	Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;		
KW	KW	HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.		
OS	XX	Homo sapiens.		
XX	XX	FR2751658-A1.		
XX	PN	30-JAN-1998.		
XX	PD	26-JUL-1996; 96FR-0009477.		
XX	PF	26-JUL-1996; 96FR-0009477.		
XX	PR	(INSP) INST PASTEUR.		
XX	PA	Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;		
XX	PI	WPI: 1998-123039/12.		
XX	DR	Human stromal cell-derived chemokine, SDF-1 - useful for treating		
XX	PT	human immunodeficiency virus infection		
XX	PS	Claim 5; Page 29; 48pp; French.		
XX	XX	The invention relates to peptides which bind to a cellular receptor for		
CC	CC	CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-		
CC	CC	expressed transmembrane domain receptor), especially where the		
CC	CC	peptide is human chemokine SDF-1. The peptide can be used to treat or		
CC	CC	prevent HIV infections, optionally together with reverse transcriptase		
CC	CC	inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4		
CC	CC	receptor antagonists, immunotherapy agents, agents for treating HIV-		
CC	CC	associated opportunistic infections and/or other CXC or CC chemokines,		
CC	CC	especially RANTES, MIP-1 alpha, MIP-1 beta or MCP1. The peptide can be		
CC	CC	used to detect anti-SDF-1 antibodies in biological fluids. This		
CC	CC	sequence represents a specifically claimed peptide which binds to the		
CC	CC	CXCR4 receptor.		
XX	SO	Sequence 68 AA;		
XX	XX	Query Match 97.8%; Score 351; DB 19; Length 68;		
XX	XX	Best Local Similarity 98.5%; Pred. No. 1.4e-38;		
XX	XX	Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1	KGVSLSYRCRCRFEESHVARAVKHLKLTIPNCALQIVARLKNNNQVCIIDRLKWIQE 60		
DB	2	KPVSLSRRCRCRFEESHVARAVKHLKLTIPNCALQIVARLKNNNQVCIIDRLKWIQE 61		
QY	61	YLEKALN 67		
DB	62	YLEKALN 68		
DE	DE	N-terminal modified chemokine met-hsSDF-1 alpha.		
XX	XX	Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hsSDF-1 alpha;		
KW	KW	human; protein engineering; amino-terminal modification; mutant;		
KW	KW	HIV; infection; angiogenesis; autoimmune disease; inflammation;		
KW	KW	antiangiogenic; antiinflammatory; immunosuppressive; therapy;		
XX	XX	vaccine.		
XX	XX	RESULT 12		
XX	AC	AAV05818		
XX	AC	AAV05818 standard; Protein; 69 AA.		
XX	AC	AAV05818;		
XX	DT	02-AUG-1999 (first entry)		
XX	XX			

OS	Homo sapiens.
OS	Synthetic.
XX	
XX	MO9920759-A1.
XX	
PD	29-APR-1999.
XX	
PF	21-OCT-1998; 98WO-US22282.
XX	
PR	20-OCT-1998; 98US-015713.
PR	22-OCT-1997; 97US-0955826.
PR	27-FEB-1998; 98WO-US04002.
XX	
PA	(GEMV) GENETICS INST INC.
PI	Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
PI	Yang O;
XX	
DR	WPI: 1999-288307/24.
DR	N-PSDB: AAX25530.
XX	
PT	Modified chemokines useful for inhibiting or stimulating
PT	angiogenesis
XX	
PS	Claim 6c: Page 79; 85pp: English.
XX	
CC	The present sequence represents met-hSDF-1 alpha, i.e. human
CC	stromal cell derived growth factor-1 alpha having an added
CC	N-terminal methionine residue. DNA encoding met-hSDF-1 alpha (see
CC	AAX25530) was produced by cloning an NdeI/XbaI-restricted hSDF-1
CC	alpha PCR product into the E. coli expression vector pAL781
CC	in-frame with an ATG codon. met-hSDF-1 alpha is an example of
CC	novel N-terminal modified chemokines (see AAY05818-21) that have at
CC	least one Met residue, at least one aminoxyethylene residue or at
CC	least one GroHEK peptide (see AAY05822) covalently attached at the
CC	N-terminus. The N-terminal modified chemokines are useful for
CC	altering receptor function, inhibiting interactions between
CC	chemokine receptors and their ligands. They are used as research
CC	tools for identifying chemokine receptors, as vaccine adjuvants, as
CC	agents for the chemotactic recruitment of migratory cells, as agents
CC	for the stimulation or inhibition of angiogenesis, as agents against
CC	autoimmune diseases and inflammation, and as agents to inhibit the
CC	binding of HIV to certain receptors and the infection of
CC	susceptible cells by HIV. HIV infection is best treated with
CC	modified SDF-1 alpha and beta or MIP-1 alpha and beta.
XX	
SO	Sequence 69 AA:
OY	Query Match 97.8%; Score 351; DB 20; Length 69; Best Local Similarity 98.5%; Pred. No. 1,4e-38; Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Dd	1 KGVSLSTGPCPCRFESHVARANVKILTLNPNCALOIVARLKNRRQVCIDPKRLKIOE 60 2 KPVSLSTGPCPCRFESHVARANVKILTLNPNCALOIVARLKNRRQVCIDPKRLKIOE 61
OY	61 YLEKALN 67 Dd 62 YLEKALN 68
RESULT 13	
ID AAM50762	
AC AAM50762 standard; peptide: 72 AA.	
XX AAM50762:	
DT 27-JUL-1998 (first entry)	
XX	
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.	
XX	
KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus; HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.	

XX	Homo sapiens.
OS	
PN	FR2751658-A1.
PD	30-JAN-1998.
XX	
PF	26-JUL-1996; 96FR-0009477.
XX	
PR	26-JUL-1996; 96FR-0009477.
XX	(INSP) INST PASTEUR.
PA	Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
PI	WPI; 1998-123039/12.
DR	
XX	
PT	Human stromal cell-derived chemokine, SDF-1 - useful for treating
PT	human immunodeficiency virus infection
XX	
PS	Claim 5; Page 29; 48pp; French.
XX	
CC	The invention relates to peptides which bind to a cellular receptor for
CC	CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC	expressed transmembrane domain receptor), especially where the
CC	peptide is human chemokine SDF-1. The peptide can be used to treat or
CC	prevent HIV infections, optionally together with reverse transcriptase
CC	inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
CC	receptor antagonists, immunotherapy agents, agents for treating HIV-
CC	associated opportunistic infections and/or other CXC or CC chemokines,
CC	especially RANTES, MIP-1 alpha, MIP-1 beta or MCP1. The peptide can be
CC	used to detect anti-SDF-1 antibodies in biological fluids. This
CC	sequence represents a specifically claimed peptide which binds to the
CC	CXCR4 receptor.
XX	
SQ	Sequence 72 AA:
	Query Match 97.8%; Score 351; DB 19; Length 72;
	Best Local Similarity 98.5%; Pred. No. 1.5e-38;
	Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 KGVSLSTYRCPCRFPESSHVARANVKHLKILNTPNCALQIVARLKNNROYCIDPKLKWIOE 60 Db 1 KPVSLSYRCPCRFPESSHVARANVKHLKILNTPNCALQIVARLKNNROYCIDPKLKWIOE 60
OY	61 YLEKALN 67 Db 61 YLEKALN 67
DE	RESULT 14
ID	AAAY34093
AC	AAAY34093 standard; protein: 72 AA.
XX	
DT	29-NOV-1999 (first entry)
XX	
DE	Native stromal cell derived factor 1 (SDF-1) beta protein.
XX	
KW	CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell; interferon gamma; autoimmune disease; multiple sclerosis; cancer; angiogenesis; stromal cell derived factor 1; SDF-1.
OS	Mammalia.
XX	
PN	WO9947158-A2.
XX	
PD	23-SEP-1999.
XX	
PF	12-MAR-1999; 99WO-CA00221.
XX	
PR	13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Clark-Lewis I, Gong J, Duronio V;
XX
DR WPI: 1999-561857/47.
XX
PT Use of CXK chemokine receptor 4 for treating autoimmune disease and
XX cancer -
PS Example 1; Fig 1; 71pp; English.
XX
CC The invention relates to the use of a CXK chemokine receptor 4 (CXCR4)
CC antagonist for the manufacture of a medicament for reducing interferon
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
CC to treat or to design a medicament to treat, an autoimmune disease.
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
CC antagonists may be peptide compounds comprising a substantially purified
CC peptide fragment, analogue or a pharmacologically acceptable salt of
CC stromal cell derived factor 1 (SDF-1). The present sequence represents
CC the amino acid sequence of SDF-1 beta protein.
XX
SQ Sequence 72 AA:
Query Match 97.8%; Score 351; DB 20; Length 72;
Best Local Similarity 98.5%; Pred. No. 1.5e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KGVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
RESULT 15
AAV67595
ID AAV67595 standard; peptide: 72 AA.
XX
AC AAV67595;
XX
DT 13-JUN-2000 (first entry)
XX
DE SDF-1beta peptide sequence.
XX
KW SDF-1; CXCR4; CXK chemokine receptor 4; gamma-interferon; cancer; gout;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.
XX
OS Unidentified.
XX
XX WO200009152-A1.
XX
XX 24-FEB-2000.
XX
XX 16-AUG-1999; 99WO-CA00750.
XX
XX 14-AUG-1998; 98CA-2245224.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Clark-Lewis I, Gong J, Duronio V, Salari H;
XX
XX WPI: 2000-224175/19.
XX
XX Therapeutic composition containing CXCR4 antagonist, useful for
XX treating autoimmune disease, especially multiple sclerosis and cancer
XX

PS Disclosure; Fig 1; 88pp; English.
XX
CC The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXK chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells; particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1beta
XX peptide sequence.
SQ Sequence 72 AA:
Query Match 97.8%; Score 351; DB 21; Length 72;
Best Local Similarity 98.5%; Pred. No. 1.5e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KGVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
Search completed: January 23, 2003, 15:33:41
Job time : 29.2 secs

QY	1	KVSLSLSPCCRFEEESHVARAVKHKILINPNCALQIVAAIKNNNOVCIDPRKMIQ	60
DB	22	KPVSLSLRCCRFEEESHVARAVKHKILINPNCALQIVAAIKNNNOVCIDPRKMIQ <th>81</th>	81
QY	61	YLEKALN	67


```

      PRIOR APPLICATION DATA: JP 280505/1993
      APPLICATION NUMBER:
      FILING DATE: 14-OCT-1993
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (202)293-7060
      TELEFAX: (202)293-7860
      TELE: 6491103
      INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 93 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      US-08-674-008-5

Query Match          97.8% Score 351; DB 1; Length 93;
Best Local Similarity 98.5%; Pred. No. 6,4e-39;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY    1 KGVSLSYRCPGRFFSFHVARANVKHLKLTLPNCALQIVARLKNNRRVCDIPKLKWIDE 60
      |||||||
Db    22 KPVLSLYRCPGRFFSFHVARANVKHLKLTLPNCALQIVARLKNRRVCDIPKLKWIDE 81
      |||||||

QY    61 YLEKALN 67
      |||||||
Db    82 YLEKALN 88

RESULT 5
US-08-808-720-3
Sequence 3, Application US/08808720
Patent No. 6100387
GENERAL INFORMATION:
APPLICANT: Herrmann, Steve
APPlicant: Swanberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
NUMBER OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark
City: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-720-3

Query Match          97.8% Score 351; DB 3; Length 326;
Best Local Similarity 98.5%; Pred. No. 2.9e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1 KGVSTSYPCPCFFESHVARANVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      20 KPVSLSYPCPCFFESHVARANVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 79

OY      61 YLEKALN 67
        |||||
Db      80 YLEKALN 86

RESULT 6
US-08-808-720-1
; Sequence 1, Application US/08808720
; Patent No. 6100387
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Steve
; APPLICANT: Swander, Stephen
; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: CHEMOKINE DOMAINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,720
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne
; REGISTRATION NUMBER: P-41,323
; REFERENCE/DOCKET NUMBER: G15291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-808-720-1

Query Match          97.8%, Score 351, DB 3, Length 328;
Best Local Similarity 98.5%; Pred. No. 2,9e+38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 KGVSTSYPCPCFFESHVARANVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      22 KPVSLSYPCPCFFESHVARANVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

OY      61 YLEKALN 67
        |||||
Db      82 YLEKALN 88

RESULT 7
US-08-181-556-2
; Sequence 2, Application US/08181556
; Patent No. 5525486
; GENERAL INFORMATION:
; APPLICANT: HONDO, Tasuku
; APPLICANT: TASHIRO, Kei
; APPLICANT: TADA, Hideaki
```

TITLE OF INVENTION: PROCESS FOR CONSTRUCTING CDNA LIBRARY,
 FILE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER
 STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22313
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/181,556
 FILING DATE: 14-JAN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 5-22098
 FILING DATE: 14-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: POULOS III, James A.
 REGISTRATION NUMBER: 31714
 REFERENCE/DOCKET NUMBER: TPP/29088
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 549-7200
 TELEFAX: (703) 528-5313
 TELEX: 89-2746
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 89 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-181-556-2

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-9

Query Match 26.2%; Score 94; DB 1; Length 68;
Best Local Similarity 32.3%; Pred. No. 2.6e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVAVANKHKLINT-PNCA-LQIVARLKNNNRQVCIDPKLWIOEYLER 64
DB 2 RCQCIKTYSKRPHFKFKELRVIESGPHCANTETIVRL-SDGRLCLDPKENVQRYVER 60
QY 65 AL 66
DB 61 FL 62

RESULT 13
US-08-244-702-10
Sequence 10, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578

FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-10

Query Match 26.2%; Score 94; DB 1; Length 68;
Best Local Similarity 32.3%; Pred. No. 2.6e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVAVANKHKLINT-PNCA-LQIVARLKNNNRQVCIDPKLWIOEYLER 64
DB 2 RCQCIKTYSKRPHFKFKELRVIESGPHCANTETIVRL-SDGRLCLDPKENVQRYVER 60
QY 65 AL 66
DB 61 FL 62

RESULT 14
US-08-244-702-11
Sequence 11, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-11

Query Match	26.2%	Score 94;	DB 1;	Length 68;
Best Local Similarity	-32.3%	Pred. No. 2.6e-05;		
Matches	20;	Conservative	18;	Mismatches 20;
			Indels	4;
			Gaps	4;

OY

8 RCRC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNRQCVIDPKLKWIOEYLEK 64
|||:: ::||:: ::: :: ::||:: ||:

Dd

2 RCGCIKTYSKPFPHPKEIKELRVIESGPHCANTEIIVKL-SDGRELCDPKNENWQRVEK 600

QY	65	AL	66
		1	
Db	61	FL	62

RESULT 15
US-08-244-702-2
; Sequence 2, Application US/08244702
; Patent No. 5655246

APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington

COUNTRY: U.S.A.
ZIP: 20006-1812

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
MEDIUM TYPE: floppy disk

```

OPERATING SYSTEM: PC-DOS/MS-DOS

```

```
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/244,702
 FILING DATE: 27-SEP-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 ADDITIONAL NUMBERS: 08/000,000

APPLICATION NUMBER: PCJ/CAS92/0052
FILING DATE: 03-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20

TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 887-15000
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS

```

; SEQUENCE CHARACTERISTICS
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
US-08-244-702-2

```

Query Match	26.2%	Score	94	DB	1	Length	69
Best Local Similarity	32.3%	Pred. No.	2.6e-05				
Matches	20	Conservative	18	Mismatches	20	Indels	4
						Gaps	4

Qy	8	RCP	REF	SH	VAR	ANK	H	K	L	I	N	T	-	P	N	C	-	L	O	I	V	A	R	L	K	N	N	N	R	O	V	C	I	D	P	K	L	K	W	I	O	E	Y	L	E	K	64								
Db	3	R	C	C	I	K	T	S	K	P	F	H	K	P	F	I	K	E	L	R	V	I	E	S	G	P	H	C	A	N	T	E	I	V	K	-	S	D	R	E	L	C	I	D	P	K	E	N	W	Q	R	V	E	K	61

QY	65	AL	66
		1	
Db	62	FL	63

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 : Search time 6.2 Seconds
(without alignments)
218.059 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359
Sequence: 1 KGVSLSYRCPCRFESHVAR.....QVCIDPKLWIEYLEKALN 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	67	9	US-09-852-424-1
2	355	98.9	67	9	US-09-852-424-7
3	354	98.6	67	9	US-09-852-424-3
4	354	98.6	67	9	US-09-852-424-6
5	353	98.3	67	9	US-09-852-424-9
6	352	98.1	67	9	US-09-852-424-2
7	352	98.1	67	9	US-09-852-424-5
8	351	97.8	67	9	US-09-852-424-8
9	351	97.8	67	9	US-09-835-107-1
10	351	97.8	67	10	US-09-144-838-8
11	351	97.8	67	10	US-09-144-838-23
12	351	97.8	89	8	US-08-927-939-22
13	351	97.8	89	9	US-09-792-793A-32
14	351	97.8	89	10	US-09-792-793A-4
15	351	97.8	89	10	US-09-953-692-4
16	351	97.8	89	10	US-09-953-717-4
17	351	97.8	93	8	US-08-927-939-56
18	351	97.8	93	9	US-09-835-107-2
19	351	97.8	93	9	US-09-835-107-3
			93	9	US-09-792-793A-93

20	351	97.8	93	10	US-09-144-838-7	Sequence 7, Appl
21	351	97.8	93	10	US-09-919-497-95	Sequence 95, Appl
22	351	97.8	320	9	US-09-792-793A-77	Sequence 77, Appl
23	351	97.8	322	9	US-09-792-793A-78	Sequence 78, Appl
24	351	97.8	327	9	US-09-792-793A-79	Sequence 79, Appl
25	349	97.2	67	9	US-09-852-424-4	Sequence 4, Appl
26	340.5	94.8	66	9	US-09-852-424-10	Sequence 10, Appl
27	337.5	94.0	66	9	US-09-852-424-11	Sequence 11, Appl
28	335.5	93.5	66	9	US-09-852-424-12	Sequence 12, Appl
29	333.5	92.9	66	10	US-09-144-838-27	Sequence 27, Appl
30	320	89.1	68	10	US-09-144-838-51	Sequence 51, Appl
31	304	84.7	67	10	US-09-144-838-47	Sequence 47, Appl
32	300	83.6	68	10	US-09-144-838-24	Sequence 24, Appl
33	297	82.7	67	10	US-09-144-838-25	Sequence 25, Appl
34	282.5	78.7	67	10	US-09-144-838-28	Sequence 28, Appl
35	269	74.9	69	10	US-09-144-838-52	Sequence 52, Appl
36	266	74.1	68	10	US-09-144-838-53	Sequence 53, Appl
37	259.5	72.3	68	10	US-09-144-838-29	Sequence 29, Appl
38	253	70.5	68	10	US-09-144-838-48	Sequence 48, Appl
39	250	69.6	67	10	US-09-144-838-49	Sequence 49, Appl
40	246	68.5	68	10	US-09-144-838-26	Sequence 26, Appl
41	228.5	63.6	67	10	US-09-144-838-30	Sequence 30, Appl
42	228	63.5	67	10	US-09-144-838-31	Sequence 31, Appl
43	217.5	60.6	66	10	US-09-144-838-35	Sequence 35, Appl
44	215	59.9	69	10	US-09-144-838-54	Sequence 54, Appl
45	199	55.4	68	10	US-09-144-838-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-852-424-1
; Sequence 1, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
US-09-852-424-1

Query Match 100.0%; Score 359; DB 9; Length 67;
Best local similarity 100.0%; Pred. No. 6; 6e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPCAIQIYARLKNRRVVCIDPKLWIE 60
DB 1 KGVSLSYRCPCRFESHVARANKHLKILNTPCAIQIYARLKNRRVVCIDPKLWIE 60
QY 61 YEKALN 67
DB 61 YEKALN 67

RESULT 2
US-09-852-424-7
; Sequence 7, Application US/09852424

```
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-7
```

Query Match 98.9%; Score 355; DB 9; Length 67;

Best Local Similarity 98.5%; Pred. No. 1,8e-32; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALDIIVARLKNNNQVCIIDPKLKIQE 60
Db 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALDIIVARLKNNNQVCIIDPKLKIQE 60
Qy 61 YLEKALN 67
Db 61 YLEKALN 67
```

RESULT 3

```
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-3
```

Query Match 98.6%; Score 354; DB 9; Length 67;

Best Local Similarity 98.5%; Pred. No. 2,3e-32;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALDIIVARLKNNNQVCIIDPKLKIQE 60
Db 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALDIIVARLKNNNQVCIIDPKLKIQE 60
```

```
Qy 61 YLEKALN 67
Db 61 YLEKALN 67
```

RESULT 4

```
US-09-852-424-6
; Sequence 6, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (5)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-6
```

Query Match 98.6%; Score 354; DB 9; Length 67;

Best Local Similarity 98.5%; Pred. No. 2,3e-32;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALDIIVARLKNNNQVCIIDPKLKIQE 60
Db 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALDIIVARLKNNNQVCIIDPKLKIQE 60
Qy 61 YLEKALN 67
Db 61 YLEKALN 67
```

RESULT 5

```
US-09-852-424-9
; Sequence 9, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (8)
```


; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-9

Query Match 98.3%; Score 353; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 3e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
DB 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 6
US-09-852-424-2
; Sequence 2, Application US/09852424
; Patent No. US20020156034A1

; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-2

Query Match 98.1%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 3.9e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
DB 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 7
US-09-852-424-5
; Sequence 5, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-5

Query Match 98.1%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 3.9e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
DB 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 8
US-09-852-424-8
; Sequence 8, Application US/09852424
; Patent No. US20020156034A1

; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (7)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-8

Query Match 97.8%; Score 351; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 5e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
DB 1 KGVSLSTYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 9
US-09-835-107-1
; Sequence 1, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.

```

: APPLICANT: Merzouk, Ahmed
: APPLICANT: Arab, Lakhdar
: APPLICANT: Saxena, Geeta
: APPLICANT: Raves, Connie J.
: APPLICANT: Cashman, Johanne
: APPLICANT: Clark-Lewis
: APPLICANT: Salati, Hassan
: TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
: FILE REFERENCE: SMAR012
: CURRENT APPLICATION NUMBER: US/09/835,107
: CURRENT FILING DATE: 2001-08-20
: PRIOR APPLICATION NUMBER: CA 2,305,036
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/232,425
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: CA 2,335,109
: PRIOR FILING DATE: 2001-02-23
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: SDF-1 alpha
US-09-835-107-1

```

```

Query Match          97.8%; Score 351; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 5e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67

```

```

RESULT 10
US-09-144-838-8
: Sequence 8, Application US/09144838A
: Patent No. US20020051996A1
: GENERAL INFORMATION:
: APPLICANT: Siani, Michael A.
: APPLICANT: Wilken, Jill
: APPLICANT: Simon, Reyna
: APPLICANT: Kent, Stephen B.H.
: TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
: FILE REFERENCE: GRN-020/01US
: CURRENT APPLICATION NUMBER: US/09/144,838A
: CURRENT FILING DATE: 1998-08-31
: EARLIER APPLICATION NUMBER: US 60/057,620
: EARLIER FILING DATE: 1997-09-04
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 8
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8

```

```

Query Match          97.8%; Score 351; DB 10; Length 67;
Best Local Similarity 98.5%; Pred. No. 5e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60

```

```

QY 61 YLEKALN 67
Db 61 YLEKALN 67

```

```

RESULT 11
US-09-144-838-23
: Sequence 23, Application US/09144838A
: Patent No. US20020051996A1
: GENERAL INFORMATION:
: APPLICANT: Siani, Michael A.
: APPLICANT: Wilken, Jill
: APPLICANT: Simon, Reyna
: APPLICANT: Kent, Stephen B.H.
: TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
: FILE REFERENCE: GRN-020/01US
: CURRENT APPLICATION NUMBER: US/09/144,838A
: CURRENT FILING DATE: 1998-08-31
: EARLIER APPLICATION NUMBER: US 60/057,620
: EARLIER FILING DATE: 1997-09-04
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 23
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-23

```

```

Query Match          97.8%; Score 351; DB 10; Length 67;
Best Local Similarity 98.5%; Pred. No. 5e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67

```

```

RESULT 12
US-08-927-939-22
: Sequence 22, Application US/08927939
: Patent No. US20010006640A1
: GENERAL INFORMATION:
: APPLICANT: Granger, David J.
: APPLICANT: Tatalick, Lauren Marie
: TITLE OF INVENTION: Compounds and methods to inhibit or
: TITLE OF INVENTION: augment an inflammatory response.
: FILE REFERENCE: 295.022US1
: CURRENT APPLICATION NUMBER: US/08/927,939
: CURRENT FILING DATE: 1997-09-11
: NUMBER OF SEQ ID NOS: 83
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 22
: LENGTH: 89
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-927-939-22

```

```

Query Match          97.8%; Score 351; DB 8; Length 89;
Best Local Similarity 98.5%; Pred. No. 6.5e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 60
Db 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALOIVARLKNNNROYCIDPKLWIOE 81
QY 61 YLEKALN 67

```

DB 82 YLEKALN 88

RESULT 13

US-09-792-793A-32
; Sequence 32, Application US/09792793A
; Patent No. US20020168370A1

; GENERAL INFORMATION:

; APPLICANT: McDonald, John R.

; APPLICANT: Coggin, Philip

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND

; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

; FILE REFERENCE: 25020-601D

; CURRENT APPLICATION NUMBER: US/09/792,793A

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: Patent Ver. 2.0

; SEQ ID NO 32

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived

; OTHER INFORMATION: Factor-1-Alpha (SDF-1-Alpha)

; PUBLICATION INFORMATION:

; JOURNAL: Genomics

; VOLUME: 28

; PAGES: 495-500

; DATE: 1995

US-09-792-793A-32

Query Match

Best Local Similarity 97.8%; Score 351; DB 9; Length 89;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KCVSLSYRCPCRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

DB 22 KCVSLSYRCPCRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

OY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 14

US-09-953-692-4
; Sequence 4, Application US/09953692

; Patent No. US20020107195A1

; GENERAL INFORMATION:

; APPLICANT: Shalley, Gupta K.

; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(

; FILE REFERENCE: P50676C1

; CURRENT APPLICATION NUMBER: US/09/953,692

; CURRENT FILING DATE: 2001-09-17

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/093,596

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Human

US-09-953-692-4

Query Match

Best Local Similarity 97.8%; Score 351; DB 10; Length 89;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KCVSLSYRCPCRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

DB 22 KCVSLSYRCPCRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

OY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 15

US-09-953-717-4

; Sequence 4, Application US/09953717

; Patent No. US20020107196A1

; GENERAL INFORMATION:

; APPLICANT: Shalley, Gupta K.

; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(

; FILE REFERENCE: P50676D1

; CURRENT APPLICATION NUMBER: US/09/953,717

; CURRENT FILING DATE: 2001-09-17

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/093,596

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Human

US-09-953-717-4

Query Match

Best Local Similarity 97.8%; Score 351; DB 10; Length 89;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KCVSLSYRCPCRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

DB 22 KCVSLSYRCPCRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

OY 61 YLEKALN 67

DB 82 YLEKALN 88

Search completed: January 23, 2003, 15:38:00
Job time : 6.2 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds

(without alignments)
555.259 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359

Sequence: 1 KGVSLSYRCPCRFESHVAR.....QVCIDPKLKWIEYLEKALN 67

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351	97.8	93	2	G01540
2	350	97.5	89	2	A53497
3	350	97.5	89	2	I53416
4	350	97.5	93	2	I81182
5	101	28.1	101	2	I48148
6	98	27.3	95	2	JN0841
7	94	26.2	99	2	A37034
8	93	25.9	101	2	S42496
9	92	25.6	103	2	A53096
10	91.5	25.5	96	2	A32954
11	90.5	25.2	91	1	A46539
12	88.5	24.7	96	2	JN0572
13	88	24.5	101	2	I46871
14	88	24.5	120	2	I48147
15	85.5	23.8	91	1	A28815
16	85.5	23.8	100	2	JH0200
17	85	23.7	109	2	A54678
18	82.5	23.0	75	2	A54188
19	81.5	22.7	75	2	B54188
20	81.5	22.7	92	2	I53222
21	81.5	22.7	119	2	J42881
22	81	22.6	120	2	JF0177
23	81	22.6	148	1	A30209
24	81	22.6	148	1	S07723
25	80.5	22.4	100	2	S21467
26	80.5	22.4	100	2	I55614
27	79.5	22.1	107	2	B38290
28	79.5	22.1	107	2	A28414
29	78.5	21.9	101	2	B28414

30	78.5	21.9	132	2	A57325
31	77.5	21.6	114	2	A55010
32	77.5	21.6	117	2	B44253
33	76.5	21.3	103	2	A26736
34	76.5	21.3	103	2	I50417
35	75.5	21.0	870	2	A41130
36	74.5	20.8	96	2	I48099
37	74	20.6	92	2	A32393
38	73.5	20.5	107	2	JH0281
39	72.5	20.2	126	2	A35766
40	72	20.1	96	2	JC2478
41	71.5	19.9	128	1	TGHU
42	70.5	19.6	53	2	I64831
43	70.5	19.6	90	2	S69133
44	69.5	19.4	98	2	I59277
45	69.5	19.4	104	1	PFH04A

ALIGNMENTS

RESULT 1
G01540
cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C:Accession: G01540
R:Spotila, L.D.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07697
A:Accession: G01540
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-93 <SPO>
A:Cross-references: EMBL:U16752; NID:q1272194; PID:g571508
C:Superfamily: beta-thromboglobulin

Query Match 97.8%; Score 351; DB 2; Length 93;
Best Local Similarity 98.5%; Pred. No. 5.5e-36;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNNNROYCIDPKLWIOE 60
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNNNROYCIDPKLWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-references: GB:ID21072; NID:9413905; PIDN:BAA04648.1; PID:9468457
R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins.
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I59582
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>

A:Cross-references: GB:L12029; NID:g393179; PIDN:AAA40100.1; PID:g393180
 C:Genetics:
 A:Gene: SDF-1-alpha
 C:Superfamily: beta-chromoglobulin
 C:Keywords: cytokine

Query Match 97.5%; Score 350; DB 2; Length 89;
 Best Local Similarity 97.0%; Pred. No. 7e-36;
 Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
 DB 22 KPVSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 3

Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I53416
 R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
 Exp. Cell Res. 215, 284-293, 1994
 A:Title: Molecular cloning of TP81, a gene whose expression is repressed by the tumor

A:Reference number: I53416; MUID:95073497; PMID:7982471

A:Accession: I53416

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: GB:S74318; NID:g786393; PIDN:AAB32650.1; PID:g786394

C:Genetics:

A:Gene: TP81

C:Superfamily: beta-chromoglobulin

Query Match 97.5%; Score 350; DB 2; Length 89;
 Best Local Similarity 97.0%; Pred. No. 7e-36;
 Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
 DB 22 KPVSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 4

Interleukin-8

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I81182

R:Tashiro, K.; Tada, H.; Heller, R.; Shirozu, M.; Nakano, T.; Honjo, T.
 Science 261, 600-603, 1993

A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I mem

A:Reference number: I59582; MUID:93342488; PMID:8342023

A:Accession: I81182

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-93 <RES>

A:Cross-references: GB:L12030; NID:g393181; PIDN:AAA40101.1; PID:g393182

C:Genetics:

A:Gene: SDF-1-beta

C:Superfamily: beta-chromoglobulin

Query Match 97.5%; Score 350; DB 2; Length 93;
 Best Local Similarity 97.0%; Pred. No. 7.3e-36;
 Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 60
 DB 22 KPVSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 81

QY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 5

Interleukin-8

C:Species: Canis lupus familiaris (dog)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995

C:Accession: JN0841

R:Shikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
 Gene 131, 305-306, 1993

A:Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene

A:Reference number: JN0841; MUID:94010328; PMID:7916715

A:Accession: JN0841

A:Molecule type: DNA

A:Residues: 1-95 <ISH>

A:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is 1

C:Genetics:

A:Introns: 22/1; 67/2

C:Superfamily: beta-chromoglobulin

Query Match 27.3%; Score 98; DB 2; Length 95;
 Best Local Similarity 34.8%; Pred. No. 7.3e-05;
 Matches 23; Conservative 15; Mismatches 20; Indels 8; Gaps 4;

QY 3 VSLSTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 57
 DB 28 VSSLTRPCRFESHVARANVKHLKTLNTPNCALQIVARLKNNRQVCIDPKLKWIOE 84
 QY 58 IOEYLE 63
 DB 85 VOKVVO 90

A:Molecule type: mRNA
A:Residues: 1-99 <RED>
A:Cross-references: GB:M17017; NID:g179579; PIDN:AAA35611.1; PID:g179580
R:kusner, D.J.; Liebers, E.L.; Nowinski, R.C.; Konieczkowski, M.; King, C.H.; Sedor, J.
Kidney Int. 39, 1240-1248, 1991
A>Title: cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells
A:Reference number: I37902; MUID:91374977; PMID:1895676
A:Accession: I37902
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-97 <RED>
A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
R:Alouni, S.; Gaertner, H.F.; Mermod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; PR
Eur J. Biochem. 227, 328-334, 1995
A>Title: A flavonoid, interleukin-8 receptor probe produced by targeted labelling at t
A:Reference number: S67519; MUID:95154308; PMID:7851404
A:Accession: S67519
A:Molecule type: mRNA
A:Residues: 1-99 <ALO>
C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
C:Comment: This protein is variably processed at the amino end. The major form differs i
C:Genetics:
A:Gene: GDB:IL8
A:Cross-references: GDB:I20099; OMIM:146930
A:Map position: 4q13-q21
A:Introns: 22/1; 67/2; 95/2
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation
F:1-20/domain: signal sequence #status predicted <SIG>
F:23-99/product: interleukin-8, minor form #status experimental <MATA>
F:28-99/product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen

Query Match 26.2%; Score 94; DB 2; Length 99;
Best Local Similarity 32.3%; Pred. No. 0.00024;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

Oy 8 RCPC-RFEESHVARNNVHLKTLNT-PNCA-LQIYARLKNNROYCIDPKLKWIOEYLEK 64
Db 33 RCQCIRTKYSKPFPFKFIKELRVIESGPHCANTEITVLK-SDGRELCDPKENVORVEK 91

Oy 65 AL 66
Db 92 FL 93

RESULT 8
S42496
interleukin-8 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-Jan-2001
C:Accession: S42496; I46997
R:Leestdaels, I.; Greenlund, T.; Arnaud, P.; Morneux, J.F.; Cordier, G.
submitted to the EMBL Data Library, March 1994
A:Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain re
A:Reference number: S42496
A:Accession: S42496
A:Molecule type: mRNA
A:Residues: 1-101 <LEG>
A:Cross-references: EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254
R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A>Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte
A:Reference number: I46997; MUID:95137691; PMID:7835984
A:Accession: I46997
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-101 <STRD>
A:Cross-references: GB:S74436; NID:g786590; PIDN:AAB33241.1; PID:g786591
C:Genetics:
A:Gene: IL-8
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation

```

F:1-20/Domain:signal sequence #status predicted <SIG>
F:21-101/Product: interleukin-8 #status predicted <MAT>

Query Match      25.9%; Score 93; DB 2; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00032;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

OY      3 VSLSRRCRCRFESFVAAN---VKHLKI LNT-PMCA-LQIVARLKNNRNOVCIDPKLKW 57
          || || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      28 MSTELRCQC--IKTHSTPFHPRFKTELKRVISGPHCENSEITIVLV-NGKEVCIDPKKEW 84
          : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

OY      58 IOEYLEKAL 66
          : | : : |
DB      85 VQKVQAF 93

RESULT 9
A:53096
interleukin-8 precursor - pig
N:Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Jun-1995 #sequence,revision 02-Jun-1995 #text-change 19-Jan-2001
C:Accession: A53096; A44253
R:Lin, G.; Pearson, A.E.; Sammurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta
J. Biol. Chem. 269, 77-85, 1994
A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba
A:Reference number: A53096; MUID:94103307; PMID:8276881
A:Accession: A53096
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <LIN>
A:Cross-references: GB:M86923; NID:g164520; PIDN:AA16616.1; PID:g164521
R:Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kujper, J.L.; Forstrom,
Biochemistry 13, 10483-10490, 1992
A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotac
A:Reference number: A44253; MUID:93041741; PMID:1420165
A:Accession: A44253
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-22, 'D', '24-103 <GOO>
A:Cross-references: GB:M9367; NID:g1235611
A:Experimental source: alveolar macrophage
A:Note: sequence extracted from NCBI backbone (NCBI:117415, NCBI:117416)
C:Keywords: chemotaxis; cytokine; inflammation
C:Superfamily: beta-chromoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-103/Product: interleukin-8 #status predicted <MAT>

Query Match      25.6%; Score 92; DB 2; Length 103;
Best Local Similarity 31.8%; Pred. No. 0.00044;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

OY      3 VSLSRRCRCRFESFVAAN---VKHLKI LNT-PMCA-LQIVARLKNNRNOVCIDPKLKW 57
          || || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      28 VSAELRCQC--INTHSTPFHPRFKTELKRVISGPHCENSEITIVLV-NGKEVCIDPKKEW 84
          : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

OY      58 IOEYLE 63
          : | : :
DB      85 VQKVQ 90

RESULT 10
A:32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence,revision 20-Oct-1989 #text-change 20-Aug-1999
C:Accession: A32954; JH0081
R:Quenendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro
A:Reference number: A32954; MUID:89139485; PMID:2917992

```


A:Accession: A32954
A:Molecule type: mRNA
A:Residues: 1-96 <CON>
A:Cross-references: GB:J04596; NID:g201042; PIDN:AAA0131.1; PID:g201043
R:Ryssek, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A>Title: Cloning and sequence of a secretory protein induced by growth factors in mouse
A:Reference number: JH0081; MUID:69078502; PMID:2909392
A:Accession: JH0081
A:Molecule type: mRNA
A:Residues: 1-96 <RVS>
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C:Genetics:
A:Map position: 5
C:Superfamily: beta-thromboglobulin
C:Keywords: extracellular protein
F:1-24/Domain: signal sequence
F:25-96/Product: gro-alpha #status predicted <MNT>
Query Match 25.5% Score 91.5 DB 2 Length 96;
Best Local Similarity 32.8% Pred. No. 0.00047;
Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;
OY 8 RCPCFESHVARAVKHLKIT-NTPNCA-LQIYARLKNNROYCIDPKLWIOYLEKA 65
Db 32 RCOQLTQTAGIHKLKNTQSLKVLPSGPCTQTEVIATLK-NGREACLDPEAPLVOKYOKM 90
OY 66 L 66
Db 91 L 91
RESULT 11
A46539
monocyte chemoattractant cytokine RANTES precursor - mouse
N:Alternate names: MURantes
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
C:Accession: I48875; A46539; I48654; I56970
R:Danoff, T.M.; Lallier, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.
J. Immunol. 152, 1182-1189, 1994
A>Title: Cloning, genomic organization, and chromosomal localization of the Scy5 gene
A:Reference number: I48875; MUID:94132613; PMID:7507961
A:Accession: I48875
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-91 <DAN>
A:Cross-references: EMBL:U02298; NID:g460090; PIDN:AAI8302.1; PID:g460091
R:Schall, T.J.; Simpson, N.J.; Max, J.Y.
Eur. J. Immunol. 22, 1477-1481, 1992
A>Title: Molecular cloning and expression of the murine RANTES cytokine: structural and
A:Reference number: A46539; MUID:92289805; PMID:1376260
A:Accession: A46539
A:Molecule type: mRNA
A:Residues: 1-18, A', 20-91 <SCH>
A:Cross-references: GB:S37648; NID:g250207; PIDN:AAB22330.1; PID:g250208
A:Experimental source: macrophage cell line PUS-1.8
A:Note: sequence extracted from NCBI backbone (NCBI:J06768, NCBI:P106770)
R:Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.
Mol. Cell. Biol. 14, 2914-2925, 1994
A>Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region
A:Reference number: I48654; MUID:94217689; PMID:7513046
A:Accession: I48654
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-91 <SHI>
A:Cross-references: EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206
R:Neilson, E.G.; Krensky, A.
Kidney Int. 41, 220-225, 1992
A>Title: Isolation and characterization of cDNA from renal tubular epithelium encoding p
A:Reference number: I56970; MUID:92277990; PMID:1375672
A:Accession: I56970
A:Status: translated from GB/EMBL/DBJ

Query Match 25.2% Score 90.5; DB 1; Length 91:
Best Local Similarity 38.2%; Pred. No. 0.00059;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Db

10 PCRFESHVA--RANVKHLKILNTPNCALQIVARLKNRRNVOCIDPKLKMIQEVYL 62
||| : |||| : | : |||| : |||| :
32 PCCFAYLSLALPRAHVKEY-FYTSKSCSNLAIVFYTRNRQVCANPEKKWQVEYI 85

RESULT 12
JN0572

A:Title: chemotactic factor-induced neutrophil chemoattractant precursor - rat
A:Alternates names: CINC; cytokine-induced neutrophil chemoattractant; Interleukin-8-1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JN0572; J01519; A34481; A48988; B48988; S51214
R:Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsurufuji, S.; F
Gene 126, 285-286, 1993

A:Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
A:Reference number: JN0572; MUID:93246259; PMID:8482545
A:Accession: JN0572

A:Molecule type: DNA
A:Residues: 1-96 <KON>

A:Cross-references: DDBJ:D11445; NID:G931854; PIDN:BAA02009.1; PID:9220755

R:Huang, S.; Paulauskis, J.D.; Kobzik, L.
Biochem. Biophys. Res. Commun. 184, 922-929, 1992

A:Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
A:Reference number: J01519; MUID:92246987; PMID:1374243
A:Accession: J01519

A:Molecule type: mRNA
A:Residues: 1-32, 'S', '34'-96 <HUA>

A:Cross-references: GB:M86536

A:Experimental source: alveolar macrophage

A>Note: The authors translated the codon AGT for residue 33 as Cys, AAC for residue 4
R:Watanabe, K.; Konishi, K.; Fujioka, M.; Kinoshita, S.; Nakagawa, H.
J. Biol. Chem. 264, 19559-19563, 1989

A:Title: The neutrophil chemoattractant produced by the rat kidney epithelial cell 1
A:Reference number: A34481; MUID:90062049; PMID:2684956
A:Accession: A34481

A:Molecule type: protein
A:Residues: 25-96 <MAT>

R:Nakagawa, H.; Ikese, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watan
Biochem. Pharmacol. 45, 1429-1430, 1993

A:Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK
A:Reference number: A48988; MUID:93228656; PMID:8471066
A:Accession: A48988

A>Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NAK>

A:Experimental source: kidney, NRK-49F fibroblasts
A>Note: sequence extracted from NCBI backbone (NCBIP:129132)
A:Accession: B48988

A>Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NAZ>

A:Experimental source: kidney, NRK-49F fibroblasts
A>Note: sequence extracted from NCBI backbone (NCBIP:129131)
R:Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsurufuji, S.
FEBS Lett. 354, 207-212, 1994

A:Title: The three dimensional structure of rat cytokine CINC/Gro in solution by homo
A:Reference number: S51214; MUID:95046333; PMID:7957925
A:Contents: annotation; conformation by (1)H-NMR, residues 25-96

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 ; Search time 6 Seconds

(without alignments)
463.152 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359

Sequence: 1 KGVSLSYRCPGCRFFESHVAR.....QVCIDPKLKNIQEYLEKALN 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	351	97.8	93	SDFL_FELCA	O62657 felis sapien
2	351	97.8	93	SDFL_HUMAN	P48061 mus sapien
3	350	97.5	89	SDFL_MOUSE	P40224 mus musculu
4	101	28.1	101	IL8_CANFA	P41324 canis famill
5	101	28.1	101	IL8_CANPO	P48113 canis porce
6	98	27.3	101	IL8_FELCA	O9X5X5 felis silve
7	94	26.2	99	IL8_HUMAN	P10145 h interleuk
8	93	25.9	101	IL8_SHEEP	P36925 ovis aries
9	92	25.6	103	IL8_PIG	P26894 sus scrofa
10	91.5	25.5	96	GRO_MOUSE	P12850 mus musculu
11	91	25.3	101	IL8_MACMO	P31495 macaca mula
12	90.5	25.2	91	SY05_MOUSE	P30882 mus musculu
13	90.5	25.2	92	SY05_RAT	P50231 rattus norv
14	90	25.1	101	IL8_BOVIN	P79255 bos taurus
15	90	25.1	130	SY05_RAT	P97885 rattus norv
16	88.5	24.7	96	GRO_RAT	P14095 rattus norv
17	88	24.5	101	IL8_RABIT	P18874 oryctolagus
18	88	24.5	120	SY02_CANPO	O08782 canis porce
19	87.5	24.4	91	SY05_CANPO	P97272 canis porce
20	87	24.2	101	IL8_CERTO	P46653 cercocebus
21	85.5	23.8	50	SY05_PIG	O20288 sus scrofa
22	85.5	23.8	91	SY05_MOUSE	P13501 homo sapien
23	85.5	23.8	100	MIP2_MOUSE	P10889 mus musculu
24	85	23.7	99	SY07_HUMAN	P80098 homo sapien
25	82.5	23.0	114	SZ06_HUMAN	P80162 homo sapien
26	81.5	22.7	71	GRO1_RABIT	P30782 oryctolagus
27	81.5	22.7	92	SY03_RAT	P50229 rattus norv
28	81.5	22.7	112	SY06_BOVIN	P80221 bos taurus
29	81.5	22.7	119	SZ07_PIG	P43030 sus scrofa
30	81	22.6	148	SY02_MOUSE	P10148 mus musculu
31	81	22.6	148	SY02_RAT	P14844 rattus norv
32	80.5	22.4	100	MIP2_RAT	P30348 rattus norv
33	80	22.3	89	SY18_HUMAN	P55774 h small ind

34	80	22.3	120	1	SY16_HUMAN	O15467 h small ind
35	79.5	22.1	107	1	GRO_HUMAN	P09341 homo sapien
36	79.5	22.1	107	1	M12B_HUMAN	P19876 homo sapien
37	78.5	21.9	91	1	SY05_BOVIN	O97919 bos taurus
38	78.5	21.9	97	1	SY08_MOUSE	O92121 mus musculu
39	78.5	21.9	101	1	GRO_CRIGR	P09340 cricetus
40	78.5	21.9	132	1	SZ05_MOUSE	P50228 mus musculu
41	78	21.7	109	1	SZ13_HUMAN	O43927 homo sapien
42	78	21.7	119	1	SY24_MOUSE	O91kc0 mus musculu
43	77.5	21.6	114	1	SZ05_HUMAN	P42830 homo sapien
44	77.5	21.6	117	1	AMC2_PIG	P22952 sus scrofa
45	77	21.4	98	1	SY13_HUMAN	O99616 homo sapien

ALIGNMENTS

```

RESULT 1
SDFL_FELCA
ID SDFL_FELCA STANDARD: PRT: 93 AA.
AC O62657:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN SDF1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA MEDLINE=96450506; PubMed=9777331;
RX Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;
RT "Molecular cloning and sequencing of feline stromal cell-derived
RT factor-1 alpha and beta."
RL Eur. J. Immunogenet. 23:303-305(1998).
CC -!- FUNCTION: CHEMOKINE-INDUCED T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AB011966; BAA28602.1; -
DR HSRP: P48061.1SDP.
DR InterPro: IPR001089; CXC-chemokine-smll.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 93
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPIC 90 93
SQ SEQUENCE 93 AA: 10581 MW: 44RC763711E9B37 CRC64;
Query Match Score 351; DB 1; Length 93;
Best Local Similarity 98.5%; Pred. No. 3.2e-36;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 KGVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLNNNOVCIDPKLKWIOE 60
 DB 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLNNNOVCIDPKLKWIOE 81
 OY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 2
 SDF1_HUMAN STANDARD: PRT: 93 AA.
 ID SDF1_HUMAN
 AC P48061;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (hIRH).
 GN SDF1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Spolia L.D.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96039262; PubMed=7490086;
 RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
 RA Shiohara T., Honjo T.;
 RT "Structure and chromosomal localization of the human stromal cell-derived factor 1 (SDF1) gene";
 RL Genomics 28:495-500(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Liver;
 RA Begun N.A., Barnard G.F.;
 RT "Nucleotide sequence of hIRH, human Interleukin reduced in hepatomas";
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP STRUCTURE BY NMR OF 22-88.
 RX MEDLINE=98046030; PubMed=9384579;
 RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A., Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D., Clark-Lewis I.;
 RT "Solution structure and basis for functional activity of stromal cell-derived factor-1; dissociation of CXCR4 activation from binding and inhibition of HIV-1";
 RL EMBO J. 16:6996-7007(1997).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
 RX MEDLINE=98284037; PubMed=9618518;
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A., Lolis E.;
 RT "Crystal structure of chemically synthesized [N3A] stromal cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin' coreceptor";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
 RT coreceptor";
 RT "FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT NOT NEUTROPHILS.
 -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
 -1- ARE PRODUCED BY ALTERNATIVE SPLICING.
 -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DB 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLNNNOVCIDPKLKWIOE 81
 OY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 3
 SDF1_MOUSE STANDARD: PRT: 89 AA.
 ID SDF1_MOUSE
 AC P40224;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating factor) (TISF).
 GN SDF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94181581; PubMed=8134392;
 RA Nagasawa T., Kikutani H., Kishimoto T.;
 RT "Molecular cloning and structure of a pre-B-cell growth-stimulating factor";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93342488; PubMed=8342023;
 RA Tashiro K., Tada H., Heikler R., Shirozu M., Nakano T., Honjo T.;
 RT "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins";
 RL Science 261:600-603(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95073497; PubMed=7982471;
 RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

Query Match 97.8%; Score 351; DB 1; Length 93;
 Best Local Similarity 98.5%; Pred. No. 3; 2e-36;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLNNNOVCIDPKLKWIOE 60
 DB 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLNNNOVCIDPKLKWIOE 81
 OY 61 YLEKALN 67
 DB 82 YLEKALN 88

FT CHAIN 1 19 POTENTIAL.
 FT DISULFID 20 93 STROMAL CELL-DERIVED FACTOR 1.
 FT DISULFID 30 55
 FT DISULFID 32 71
 FT VARSPLIC 90 93 MISSING (IN ISOFORM ALPHA).
 SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44EBD CRC64;

RA Weinstein I.B.;
 RT "Molecular cloning of TPAP1, a gene whose expression is repressed by
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
 RL Exp. Cell Res. 215:284-293(1994).
 RN [4]
 RC SEQUENCE FROM N.A.
 RC STRAIN-AKR/J;
 RL Nomura M., Nakata Y., Nose M., Akashi M., Suzuki G.;
 Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CHEMOTACTICALLY ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 NOT NEUTROPHILS.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
 PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
 STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
 ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE INTERCINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D21072; BAA04648.1; -;
 CC EMBL: L12029; AAA40100.1; -;
 CC EMBL: L12030; AAA40101.1; -;
 CC EMBL: S74318; AAB32650.1; -;
 CC EMBL: D43804; BAA07862.1; -;
 CC EMBL: D43805; BAA07863.1; -;
 CC PIR: A53497; A53497.
 CC HSP: P48061; ISDF.
 CC MGD: MGI:103556; Sdfl.
 CC InterPro: IPR001089; CXCL; chemokine_sm1.
 CC InterPro: IPR001811; Chemokine_IL8.
 CC Pfam: PF00048; IL8; 1.
 CC SMART: SM00199; SCY; 1.
 CC ProSite: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 CC Kyr Cycle: Chemotaxis; Growth factor; Signal; Alternative splicing.
 CC SIGNAL 1 19 STROMAL CELL-DERIVED FACTOR 1.
 CC CHAIN 20 89 POTENTIAL.
 CC FT DISULFID 30 55 BY SIMILARITY.
 CC FT DISULFID 32 71 BY SIMILARITY.
 CC FT VARSPLIC 89 89 K -> KRKM (IN ISOFORM BETA).
 CC SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;
 Query Match 97.5%; Score 350; DB 1; Length 89;
 Best Local Similarity 97.0%; Pred No. 4e-36;
 Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KCVSLSYRCPRFFESHVARVANKHLINTPCALQIYARLKNRRVOCIDPKLWIOE 60
 Db 22 KPVSLSYRCPRFFESHIRAVANKHLINTPCALQIYARLKNRRVOCIDPKLWIOE 81
 Oy 61 YLEKALN 67
 Db 82 YLEKALN 88
 RESULT 4
 IL8_CANFA
 ID IL8_CANFA STANDARD: PRT: 101 AA.
 AC P41324;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC MEDLINE=94010328; PubMed=7916715;
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.;
 RT "Cloning of a canine gene homologous to the human
 Interleukin-8-encoding gene.";
 RL Gene 131:305-306(1993).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=95127913; PubMed=7827282;
 RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,
 RA Gotsuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshitake K.,
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;
 RT "Molecular cloning and expression of canine interleukin 8 cDNA.";
 RL Cytokine 6:455-461(1994).
 RN [3]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Monrel; TISSUE=Jugular vein;
 RX MEDLINE=95114148; PubMed=7814650;
 RA Kukiela G.L., Smith W.C., Larosa G.J., Manning A.M.,
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,
 RA Michael L.H., Rot A., Entman M.L.;
 RT "Interleukin-8 gene induction in the myocardium after ischemia and
 reperfusion in vivo.";
 RL J. Clin. Invest. 95:89-103(1995).
 RN [4]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Beagle;
 RX MEDLINE=97230298; PubMed=9119462;
 RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;
 RT "Borrelia burgdorferi migrates into joint capsules and causes an up-
 regulation of interleukin-8 in synovial membranes of dogs
 experimentally infected with ticks.";
 RL Infect. Immun. 65:1273-1285(1997).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 RESPONSE TO AN INFLAMMATORY STIMULUS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE INTERCINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D28772; BAA05961.1; -;
 CC EMBL: D14285; BAA03246.1; -;
 CC EMBL: U010308; AAC48434.1; -;
 CC EMBL: AF048717; AAC05134.1; -;
 CC HSP: P10145; IIRK.
 CC InterPro: IPR001089; CXCL; chemokine_sm1.
 CC InterPro: IPR001811; Chemokine_IL8.
 CC Pfam: PF00048; IL8; 1.
 CC PRINTS: PR00437; SMALLCYTKCXC.
 CC SMART: SM00199; SCY; 1.
 CC ProSite: PS00471; SMALL_CYTOKINES_CXC; 1.
 CC Kyr Cycle: Chemotaxis; Inflammatory response; Signal.
 CC SIGNAL 1 22
 CC CHAIN 23 101 INTERLEUKIN-8.
 CC FT DISULFID 34 61 BY SIMILARITY.
 CC FT DISULFID 36 77 BY SIMILARITY.
 CC SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;
 Query Match 28.1%; Score 101; DB 1; Length 101;

Best Local Similarity 36.1%; Pred. No. 1.4e-05;
Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;

OY 3 VSLSYRCPREFESHVARAN---VKHLKILNT--PNCA-LOIVARLKNNNROVCIDPKLKW 57
DB 28 VSSLRCQC--IKHTSPFPFKIKELRLVIDSGPHCENSEITIVKL--EVCIDPKRKM 84

OY 58 IOE---YLEKA 65
DB 85 VQKVVEFLKKA 96

RESULT 5
ID IL8_CAVPO STANDARD; PRT; 101 AA.

AC P49113;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein 1) (NAP-1).
GN IL8.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
ON NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94065176; PubMed=7504015;

RA Yoshimura T., Johnson D.G.;
RT "CDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";
RL J. Immunol. 151:6225-6236(1993).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----

CC EMBL; L04986; AAA37049.1; -.
DR HSSP; P10145; 2IL8.
DR InterPro: IPR001089; CXCL_Chmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCX.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;

Query Match 28.1%; Score 101; DB 1; Length 101;
Best Local Similarity 35.9%; Pred. No. 1.4e-05;
Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

OY 8 RCPREFESHVARAN---VKHLKILNT--PNCA-LOIVARLKNNNROVCIDPKLKW 62
DB 33 RCQC--IKHTSPFPFKIKELRLVIDSGPHCENSEITIVKL--SDNRKCLDPKRWQDVV 89

OY 63 EKAL 66
DB 90 SMFL 93

RESULT 6
ID IL8_FELCA STANDARD; PRT; 101 AA.

AC O9XSX5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
ON NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubinger A.F., Simpson K.W., Straubinger R.K.;

RT "Feline interleukin-8 mRNA."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----

CC EMBL; AF158598; AAD40323.1; -.
DR HSSP; P10145; 1IKM.
DR InterPro: IPR001089; CXCL_Chmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCX.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11165 MW; 690D97F13EF79120 CRC64;

Query Match 27.3%; Score 98; DB 1; Length 101;
Best Local Similarity 33.3%; Pred. No. 3.2e-05;
Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSLSYRCPREFESHVARAN---VKHLKILNT--PNCA-LOIVARLKNNNROVCIDPKLKW 57
DB 28 ISSLRQC--IKHTSPFPFKIKELRLVIDSGPHCENSEITIVKL--NGKEVCIDPKRKM 84

OY 58 IOEYLE 63
DB 85 VQKVVE 90

RESULT 7
ID IL8_HUMAN STANDARD; PRT; 99 AA.

AC P10145; O9C077; O96RG6;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil
 DE chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-
 DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-
 DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emoctrakin).
 GN IL8
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88258376; PubMed=3260265;
 RA Matsushima K., Morishita K., Yoshimura T., Lavi S., Kobayashi Y.,
 RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic
 RT factor (MDNCF) and the induction of MDNCF mRNA by interleukin 1 and
 RT tumor necrosis factor.";
 RL J. Exp. Med. 167:1883-1893(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87224164; PubMed=2953813;
 RA Schmid J., Weissmann C.;
 RT "Induction of mRNA for a serine protease and a
 RT beta-thromboglobulin-like protein in mitogen-stimulated human
 RT leukocytes.";
 RL J. Immunol. 139:250-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89313739; PubMed=2664463;
 RA Kowalski J., Denhardt D.T.;
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating
 RT peptide in differentiating HL60 promyelocytes.";
 RL Mol. Cell. Biol. 9:1946-1957(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89309826; PubMed=2663993;
 RA Mukaida N., Shitoo M., Matsushima K.;
 RT "Genomic structure of the human monocyte-derived neutrophil
 RT chemotactic factor IL-8.";
 RL J. Immunol. 143:1366-1371(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ishikawa J.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Jang J.S., Kim B.E.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Riederer M.J., Carlington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 23-46.
 RX MEDLINE=89246368; PubMed=2655583;
 RA Golds E.E., Mason P., Nytkos P.;
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
 RT human synovial cells and fibroblasts.";
 RL Biochem. J. 259:585-588(1989).
 RN [9]
 RP SEQUENCE OF 23-54.
 RX MEDLINE=89279141; PubMed=2659722;
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,
 RA Mizuno S.;
 RT "Purification and partial primary sequence of a chemotactic protein
 RT for polymorphonuclear leukocytes derived from human lung giant cell
 RT carcinoma LU6SC cells.";
 RL J. Exp. Med. 169:1895-1901(1989).
 RN [10]

RP SEQUENCE OF 28-99.
 RX MEDLINE=88162914; PubMed=3279957;
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;
 RT "Structure determination of a human lymphocyte derived neutrophil
 RT activating peptide (LYNAP).";
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).
 RN [11]
 RP SEQUENCE OF 28-59.
 RX MEDLINE=88106502; PubMed=3322281;
 RA Walz A., Feveri P., Aschauer H., Baggiolini M.;
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-
 RT activating factor produced by monocytes.";
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).
 RN [12]
 RP SEQUENCE OF 28-69.
 RX MEDLINE=88097462; PubMed=3480540;
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,
 RA Oppenheim J.J., Leonard E.J.;
 RT "Purification of a human monocyte-derived neutrophil chemotactic
 RT factor that has peptide sequence similarity to other host defense
 RT cytokines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).
 RN [13]
 RP N-TERMINAL FORMS.
 RX MEDLINE=91006326; PubMed=2145175;
 RA van Damme J., Rampart M., Conling R., Decock B., van Osselaer N.,
 RA Willems J., Billiau A.;
 RT "The neutrophil-activating proteins interleukin 8 and beta-
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally
 RT processed forms.";
 RL Eur. J. Immunol. 20:2113-2118(1990).
 RN [14]
 RP N-TERMINAL FORMS.
 RX MEDLINE=89231715; PubMed=2523801;
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;
 RT "Purification of granulocyte chemotactic peptide/interleukin-8
 RT reveals N-terminal sequence heterogeneity similar to that of
 RT beta-thromboglobulin.";
 RL Eur. J. Biochem. 181:337-344(1989).
 RN [15]
 RP SYNTHESIS OF 28-99.
 RX MEDLINE=91175767; PubMed=2007144;
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,
 RA Aebersold R.;
 RT "Chemical synthesis, purification, and characterization of two
 RT inflammatory proteins, neutrophil activating peptide 1
 RT (interleukin-8) and neutrophil activating peptide.";
 RL Biochemistry 30:3128-3135(1991).
 RN [16]
 RP REVIEW.
 RX MEDLINE=92347562; PubMed=1639201;
 RA Baggiolini M., Clark-Lewis I.;
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";
 RL FEBS Lett. 307:97-101(1992).
 RN [17]
 RP STRUCTURE BY NMR.
 RX MEDLINE=90234679; PubMed=2184886;
 RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;
 RT "Three-dimensional structure of Interleukin 8 in solution.";
 RL Biochemistry 29:1689-1696(1990).
 RN [18]
 RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.
 RX MEDLINE=99148123; PubMed=10368283;
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;
 RT "Structure of a CXCR chemokine-receptor fragment in complex with
 RT interleukin-8.";
 RL Structure 7:157-168(1999).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=90216714; PubMed=2182630;
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,
 RA Wlodawer A., Weber I.T.;
 RT "Crystallization of human interleukin-8. A protein chemotactic for

DE chemotactic factor I) (AMCF-I).
GN IL8.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94103307; PubMed=8276881;
RA Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,
RA Weiss D.J., Murtough M.P.;
RT "Regulation of interleukin-8 expression in porcine alveolar
RT macrophages by bacterial lipopolysaccharide.";
RL J. Biol. Chem. 269:77-85(1994).
RN (2)
RP SEQUENCE FROM N.A.
RA Sanjanwala M.;
RL Submitted (JUL-1991) to the EMBL/Genbank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.
RC TISSUE=Lung;
RX MEDLINE=93041741; PubMed=1420165;
RA Goodman R.B., Foster D.C., Mathews S.L., Osborn S.G., Kuiper J.L.,
RA Forstrom J.W., Martin T.R.;
RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil
RT chemotactic factors I and II: Identification of porcine IL-8 and
RT another interleukin-alpha protein.";
RL Biochemistry 31:10483-10490(1992).
RN (4)
RP REVISION TO 23.
RA Goodman R.B.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN (5)
RP SEQUENCE OF 26-45.
RC STRAIN=Yorkshire;
RX MEDLINE=91217086; PubMed=1850745;
RA Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;
RT "Identification of two neutrophil chemotactic peptides produced by
RT porcine alveolar macrophages.";
RL J. Biol. Chem. 266:8455-8463(1991).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.
CC -1- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M86923; AAA16616.1;
CC EMBL: X6151; CAA43461.1;
CC EMBL: M99367; AAA92576.1;
CC PIR: A44253; A44253.
CC PIR: A39819; A39819.
CC HSP: P10145; 1IKM.
CC InterPro: IPR001089; CXCL_clnkine_sm11.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC PRINTS: PR00437; SMALLCYTKCX.
CC SMART: SMD0199; SCY; 1.
CC PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
CC Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 25
FT CHAIN 26 103 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
FT CONFLICT 33 34 RC -> CR (IN REF. 5).
FT CONFLICT 87 87 K -> KK (IN REF. 2).
SQ SEQUENCE 103 AA; 11633 MM; 9FE0E350E1928C64 CRC64;
Query Match 25.6%; Score 92; DB 1; Length 103;
Best Local Similarity 31.8%; Pred. No. 0.00017;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;
OY 3 VSLSTRPCRFESHVARN---VKHLTLNT-PNCA-LQIYARLKNNRNVCIDPKLW 57
DB 28 VSAELRCQC--INTHSTPPHPKFIKELRVIESGPHCENSEIIVKLV-NCKEYCLDPKRW 84
OY 58 IOEYLE 63
DB 85 VQKVVO 90
RESULT 10
GRO_MOUSE
ID GRO_MOUSE STANDARD: PRT: 96 AA.
AC P12850;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth regulated protein precursor (CXCL) (Platelet-derived growth
DE factor-induced protein KC) (Secretory protein NS1).
GN SCYB1 OR GRO1 OR GRO OR MGS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89139485; PubMed=2917992;
RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
RT "The platelet-derived growth factor-inducible KC gene encodes a
RT secretory protein related to platelet alpha-granule proteins.";
RL J. Biol. Chem. 264:4133-4137(1989).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=89078502; PubMed=2909392;
RA Ryseck R.P., Macdonald-Bravo H., Matriel M.-G., Bravo R.;
RT "Cloning and sequence of a secretory protein induced by growth
RT factors in mouse fibroblasts.";
RL Exp. Cell Res. 180:266-275(1989).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv.
RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,
RA Conklin M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
RN (4)
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96016008; PubMed=7561058;
RA Ohmori Y., Fukumoto S., Hamillon T.A.;
RT "Two structurally distinct kappa B sequence motifs cooperatively
RT control LPS-induced KC gene transcription in mouse macrophages.";
RL J. Immunol. 155:3593-3600(1995).
CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY
CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

CC entitles requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to: license@sib-sib.ch).
-----
CC DR EMBL; J04596; AAA40131.1; -.
CC DR EMBL; U20634; AAB03376.1; -.
CC DR EMBL; U20527; AAB03376.1; JOINED.
CC DR EMBL; S79767; -. NOT_ANNOTATED_CDS.
CC DR PIR; A32954; A32954.
CC DR PIR; JH0081; JH0081.
CC DR HSSP; P19875; IQNK.
CC DR MGD; MGI:108068; Grol.
CC DR InterPro; IPR001089; CXK_chk_kine_sm11.
CC DR InterPro; IPR001811; Chemokine_IL8.
CC DR Pfam; PF00048; IL8; 1.
CC DR PRINTS; PR00437; SMALLCYTCKXC.
CC DR SMART; SM00199; SCY; 1.
CC DR PROSITE; PS00471; SMALL_CYTOKINES_CXK; 1.
CC DR Cyclic; Growth factor; Inflammatory response; Signal.
CC FT SIGNAL 1 24 PROBABLE.
CC FT CHAIN 25 96 GROWTH REGULATED PROTEIN.
CC FT DISULFID 33 59 BY SIMILARITY.
CC FT DISULFID 35 75 BY SIMILARITY.
CC SQ SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38B45C2 CRC64;

Query Match 25.5%; Score 91.5; DB 1; Length 96;
Best Local Similarity 32.8%; Pred. No. 0.00019;
Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3.

QY 8 RCPCRFEESHVAVANKHLKIL-NTPNCA-LQIVARLKNNNRQVCDPRLKNIQIYLEKA 65
Db 32 RCGCGTGMAGHILKNLQSLKVLPSGPHCHQTEVIATLK-NGREACDIPAPLVQKIVQKM 90
QY 66 L 66
Db 91 L 91

RESULT 11
IL8_MACMU STANDARD; PRT; 101 AA.
AC P51495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=7628861;
RA Minerley J.C., Bagdoff M.P., Depeeler C.L., Keller B.T.,
RA Rapp S.R., Widomski D.L., Fretland D.J., Bolanowski M.A.;
RT "Identification and characterization of Rhesus macaque
RT Interleukin-8.";
RL Inflammation 19:313-331(1995).
CC -I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS. BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

```

-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isdb.ch/announce/>
CC or send an email to license@isdb.ch).

CC EMBL: U19849; AAA86711.1; -;
DR EMBL: U19851; AAA86713.1; -;
DR EMBL: S78555; AAA80141.2; -;
DR HSSP: P10145; 2ILB.
DR InterPro: IPR001089; CXCL_chkline_sm11.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF000048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCX.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
FT CYCLOKIN: Chemotaxis; Inflammatory response; Signal.
KW SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SO SEQUENCE 101 AA; 11320 MW; 42BCFC9C7C84B5F9 CRC64;

Query Match 25.3%; Score 91; DB 1; Length 101;
Best Local Similarity 31.7%; Pred. No. 0.00023;
Matches 19; Conservative 18; Mismatches 19; Indels 4; Gaps 4;

QY 8 RCPC-RFEESHVARNVHLKLINT-PNCA-LQIVARKNNRQYCIDPKIKIQEYLEK 64
II::: :I::: :I::: :I::: :I::: :I::: :I::: :I::: :I::: :I:::
DB 33 RCECIKYTSKEFHPIKFELRVIESGPHCANETIVKL-SDGRRLCDLPKEPMVGRAVEK 91

RESULT 12
SY05-MOUSE STANDARD; PRT: 91 AA.

AC P30882;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) ('T-cell specific RANTES
DE protein') (SIS-delta) (Murantes).
GN SCYA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=92277990; PubMed=1375672;
RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
RA Kremsky A.M., Nelson E.G.;
RT "Isolation and characterization of cDNA from renal tubular epithelium
RT encoding murine Rantes.";
RL Kidney Int. 41:220-225(1992).
RN [2]
RP MEDLINE FROM N.A.
RX MEDLINE=92289805; PubMed=1376260;
RA Schall T.J., Simpson N.J., Mak J.Y.;
RT "Molecular cloning and expression of the murine RANTES cytokine:
RT structural and functional conservation between mouse and man.";
RL Eur. J. Immunol. 22:1477-1481(1992).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=NH SWISS;
RX DANIOFF T.M., LALLEY P.A., CHANG Y.S., HEGER P.S., NELSON E.G.;
RT "Cloning, genomic organization, and chromosomal localization of the


```

RT "Cloning and sequencing of bovine Interleukin 8 cDNA isolated from
RT 1lipopolysaccharide stimulated monocytes in vitro."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S82598; AAB37483.1; -
DR EMBL; AF232704; AAF37575.1; -
DR HSSP; P10145; 1IKM.
DR InterPro; IPR001089; CXC_Chemkine_sml1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11291 MW; 061A530507906736 CRC64;

Query Match 25.1%; Score 90; DB 1; Length 101;
Best Local Similarity 30.3%; Pred. No. 0.0003;
Matches 20; Conservative 20; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSLSYRCPCRFESHVARAN---VKHLKIILNT-PNCA-LOIIVARLKNNNROYCIDPKLKW 57
DB 28 MSTELRCOC--IKTHSTPPHFKPIKELKRVESGPHCENSEITIVKLTNGN-EVCLNPKRKW 84

OY 58 IOEYLE 63
DB 85 VQKVVQ 90

RESULT 15
SZ05_RAT STANDARD; PRT; 130 AA.
AC P97885;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).
GN SCYB5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RA Keiner G.S.; Maciejewski-Lenoir D.; Lee E.D.; Maki R.A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY PARTICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS
CC BY INJURED OR INFECTED TISSUE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

```

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U90448; AAB61460.1; -
DR EMBL; P10889; 1MI2.
DR InterPro; IPR001089; CXC_Chemkine_sml1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 130 SMALL INDUCIBLE CYTOKINE B5.
FT DISULFID 50 76 BY SIMILARITY.
FT DISULFID 52 93 BY SIMILARITY.
SQ SEQUENCE 130 AA; 14263 MW; C00F6B3605524F4E CRC64;

```

```

Query Match 25.1%; Score 90; DB 1; Length 130;
Best Local Similarity 27.3%; Pred. No. 0.00039;
Matches 18; Conservative 19; Mismatches 27; Indels 2; Gaps 2;

OY 3 VSLSYRCPCRFESHVARANVKHLKIILNT-PNC-ALQIVARLKNNNROYCIDPKLWIOE 60
DB 44 VATELRVCCLTLNAPRIKPMIANLEVIAPGPHCPKVEIVAKLNQNDVCLDPOAPLKK 103

OY 61 YLEKAL 66
DB 104 VIOKIL 109

```

Search completed: January 23, 2003, 15:34:18
Job time : 7 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 ; Search time 22.6 Seconds
(without alignments)
610.848 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359
Sequence: 1 KGVSLSYRCPCRFESHVAR.....QVCIDPKLKIQEIYERKALN 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP virus:*
- 16: SP bacteriophage:*
- 17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351	97.8	92	4	Q9H554
2	343	95.5	89	11	Q9Q2D1
3	285	79.4	94	13	Q8U0U9
4	93.5	26.0	91	11	Q912L1
5	88	24.5	98	13	Q8QGV8
6	88	24.5	109	13	Q8QV59
7	83.5	23.3	134	12	Q9YVA9
8	83.5	23.3	142	12	Q91B77
9	83	23.1	104	13	Q73912
10	83	23.1	203	12	Q67634
11	80	22.3	148	11	Q9QYD7
12	79.5	22.1	101	13	Q93442
13	79.5	22.1	108	6	Q28724
14	79	22.0	97	13	Q987Q2
15	78.5	21.9	97	11	Q92318
16	78.5	21.9	363	13	Q90ZT0

17	78.5	21.9	1096	13	Q90ZT1	Q90ZT1 brachydanio
18	77.5	21.6	100	11	Q91ZK9	Q91ZK9 sigmodon hi
19	77	21.4	79	4	Q95689	Q95689 homo sapien
20	76.5	21.3	101	11	Q91Z64	Q91Z64 sigmodon hi
21	76	21.2	101	13	Q8UW91	Q8UW91 triakis scy
22	76	21.2	106	11	Q92292	Q92292 cricetus
23	75.5	21.0	883	13	Q91493	Q91493 torpedo cal
24	74.5	20.8	97	13	Q8QFP5	Q8QFP5 cyprinus ca
25	73.5	20.5	126	11	Q93J60	Q93J60 mus musculu
26	73.5	20.5	601	13	Q73928	Q73928 scyllorhinu
27	73	20.3	102	6	Q95M27	Q95M27 ovis aries
28	71	19.8	95	12	Q98158	Q98158 kaposi's sa
29	70.5	19.6	91	13	Q8Q556	Q8Q556 gallus galli
30	70	19.5	91	13	Q8Q557	Q8Q557 gallus galli
31	70	19.5	96	13	Q90825	Q90825 gallus galli
32	69.5	19.4	97	6	Q9TTS6	Q9TTS6 bos taurus
33	69.5	19.4	150	11	Q9QW66	Q9QW66 mus sp. dys
34	69.5	19.4	258	11	Q9D637	Q9D637 mus musculu
35	69.5	19.4	622	4	Q02295	Q02295 homo sapien
36	69.5	19.4	3685	4	Q14205	Q14205 homo sapien
37	69	19.2	80	4	Q14745	Q14745 homo sapien
38	69	19.2	92	6	Q85Q40	Q85Q40 felis silve
39	69	19.2	93	4	Q96168	Q96168 homo sapien
40	69	19.2	395	11	Q91V44	Q91V44 mus musculu
41	68.5	19.1	100	6	Q9TTO4	Q9TTO4 equus cabal
42	68.5	19.1	101	11	Q9EP62	Q9EP62 rattus norv
43	68	18.9	89	13	Q91B80	Q91B80 gallus galli
44	67.5	18.8	116	11	Q91Z82	Q91Z82 mus musculu
45	66	18.4	92	11	Q91Z65	Q91Z65 sigmodon hi

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	92 AA.
ID Q9H554			
AC Q9H554:			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)			
DE (Fragment).			
GN SDF1			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_TaxID=9606;			
OX RN			
RP SEQUENCE FROM N.A.			
RA Bird C.;			
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
DR EMBL: AL137026; CAC10202.1; -			
DR HSSP: P48061; ISDF.			
DR InterPro: IPR001811; Chemokine_IL8.			
DR Pfam: PF00048; IL8; 1.			
DR SMART: SM00193; SCR; 1.			
FT NON_TER			
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B44EBD20 CRC64;			
Query Match	97.8%;	Score 351;	DB 4; Length 92;
Best Local Similarity	98.5%;	Pred. No. 5e-36;	
Matches 66;	Conservative 0;	Mismatches 1;	Indels 0;
Gaps 0;			
QY 1 KGVSLSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKIOWE 60			
DB 22 KPVSLSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKIOWE 81			
QY 61 YLEKALN 67			
DB 82 YLEKALN 88			


```

SQ SEQUENCE 98 AA: 10846 MW: 495CA4839A5D8C92 CRC64;
Query Match 24.5%; Score 88; DB 13; Length 98;
Best local Similarity 27.1%; Pred. No. 0.0023;
Matches 19; Conservative 20; Mismatches 27; Indels 4; Gaps 3;

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPN--C-AIQIVARLKNNNQVCIDPKLKW 57
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 27 RSLGVSLHRCICETESRPICRIKYSVEII-SPNSHCDKTEIITATLKDGTGVELCLDPEAPW 85
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 58 IOEYLEKALN 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 86 VKRVINKLIS 95
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
Q90Y59 PRELIMINARY: PRT: 109 AA.
ID Q90Y59
AC Q90Y59;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Interleukine-8.
GN IL-8.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidel; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435923; PubMed=11551708;
RA Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;
RT "Cloning and sequence analysis of the Interleukin-8 gene from flounder
  (Paralicthys olivaceus).";
RL Gene 274:237-243(2001).
DR EMBL: AF216646; AAL05442.1;
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
SQ SEQUENCE 109 AA: 12117 MW: C7CE18986C50A6ED CRC64;

Query Match 24.5%; Score 88; DB 13; Length 109;
Best local Similarity 27.1%; Pred. No. 0.0026;
Matches 19; Conservative 20; Mismatches 27; Indels 4; Gaps 3;

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPN--C-AIQIVARLKNNNQVCIDPKLKW 57
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 26 RSLGVSLHRCICETESRPICRIKYSVEII-SPNSHCDKTEIITATLKDGTGVELCLDPEAPW 84
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 58 IOEYLEKALN 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 85 VKRVINKLIS 94
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
Q9YVA9 PRELIMINARY: PRT: 134 AA.
ID Q9YVA9
AC Q9YVA9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE VIL8 (CXC chemokine VIL8).
GN MDV003 OR MDV078.
OS Gallid herpesvirus 1,
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Marek's disease herpesvirus (strain Md5) (MDV). Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
OX NCBI_TaxID=10386, 10388, 10389;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Gallid herpesvirus 1; STRAIN-RB1B;

```

```

RA Rasschaert D., Fagnant L.;
RT "Characterisation of the BamHI I fragment of the Marek's disease virus
  RB1B strain (serotype 1).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain GA) (MDHV);
RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.;
RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain Md5) (MDV);
RX MEDLINE=20392152; PubMed=10933706;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
RL J. Virol. 74:7980-7988(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain Md5) (MDV);
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF331499; AAL58097.1;
DR EMBL: AF065430; AAC77449.1;
DR EMBL: AF243438; AAG14290.1;
DR EMBL: AF243438; AAG14256.1;
DR HSSP: P10889; IM12.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemokine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1.
SQ SEQUENCE 134 AA: 14828 MW: C859CDB86BD25190 CRC64;

Query Match 23.3%; Score 83.5; DB 12; Length 134;
Best local Similarity 25.9%; Pred. No. 0.011;
Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps 5;

QY 2 GVSLSYRCPCRFESHVARANKHLKILNTPN-----NC-AIQIV 39
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 22 GISLESIAVDKRCRC-----VKVNRPTGLPIIADVIPPGRICRTEII 67
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 40 ARLKNNNQVCIDPKLKWIOEYLEK 64
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 68 FALK-KNRKVCVDPPEAPWQDFIK 91
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
Q9IBJ7 PRELIMINARY: PRT: 142 AA.
ID Q9IBJ7
AC Q9IBJ7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE VIL-8.
GN R-LOF2.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RX MEDLINE=92237304; PubMed=1315048;
RA Jones D., Lee L., Liu J.L., Kung H.-J., Tilloston J.K.;
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
  the fos/jun oncogenes that is highly expressed in lymphoblastoid
  tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RA Lee L.F., Wu P., Sui D., Ren D., Kung H.-J.;

```

RT "The Complete UL Sequence of Serotype I Marek's Disease Virus."
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
 DR EMBL: AF147806; AAF67205.1; -
 DR EMBL: AF147806; AAF6793.1; -
 DR HSSP: P10889; IM12.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12; Chemokine_sm11.
 DR InterPro: IPR001230; Prey1_site.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCKC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
 DR SEQUENCE 142 AA; 15770 MW; 3548CEB9B29FD209 CRC64;
 SQ
 Query Match 23.3%; Score 83.5; DB 12; Length 142;
 Best Local Similarity 25.9%; Pred. No. 0.012; Mismatches 12; Indels 37; Gaps 5;
 Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps 5;
 QY 2 GVSL-----SYRCPCREFESHVARANVHKLILNTP-----NC-ALQIV 39
 DB 22 GISLESLAVDKRC-----VKVTRNPTGLGPIIADVPIPGIHRRTETI 67
 QY 40 ARKNNRQVCIDPRKMKIQLYER 64
 DB 68 FALK-KNRKVCVDEAPVWQOFIRK 91
 RESULT 9
 ID 073912 PRELIMINARY; PRT; 104 AA.
 AC 073912;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE K60 protein precursor (CXCL12 chemokine K60).
 GN K60.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MACROPHAGE LIKE;
 RA Sick C.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MDLINE=20170941; PubMed-10704244;
 RA Sick C., Schneider K., Staeheli P., Weinig K.C.;
 RL "Novel chicken CXCL12 and CXCL12 chemokines."
 RL Cytochrome 12:181-186(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RL "Mapping of a second ELR CXCL12 chemokine to chicken chromosome four."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y14971; CAA75212.1; -
 DR EMBL: AF277660; AAF6485.1; -
 DR HSSP: P02775; ITVX.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12; Chemokine_sm11.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCKC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL-CYTOKINES-CXC; 1.
 KW SIGNAL.
 GN SIGNAL.
 FT CHAIN 1 20 POTENTIAL.
 FT CHAIN 21 104 K60 PROTEIN.
 SQ SEQUENCE 104 AA; 11199 MW; 83725AB91FE18ED CRC64;
 Query Match 23.1%; Score 83; DB 13; Length 104;
 Best Local Similarity 27.5%; Pred. No. 0.01;

Matches 19; Conservative 20; Mismatches 22; Indels 8; Gaps 4;
 QY 4 SLVSRCPREFESHVARANVHKLILNTP-----PNCALQIVARLKNRQVCIDPRKMKI 58
 DB 29 AIELRCOC--LEHSHKTRIFKFIQNVNLTPSGPCKNVEVATLK-DGREYCLDPTAPW 85
 QY 59 QEYLEKALN 67
 DB 86 KLILKALD 94
 RESULT 10
 ID 067634 PRELIMINARY; PRT; 203 AA.
 AC 067634;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Eco Q protein (Fragment).
 OS Marek's disease herpesvirus (strain GA) (MDV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 NC NCBI_TaxID=10388;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GA;
 RX MEDLINE=96074534; PubMed-7491783;
 RA Peng Q., Zeng M., Bhuiyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
 RA Shitazaki Y.;
 RL "Isolation and characterization of Marek's disease virus (MDV) cDNAs
 RL mapping to the BamHI-12, BamHI-Q2, and BamHI-L fragments of the MDV
 RL genome from lymphoblastoid cells transformed and persistently infected
 RL with MDV."
 RL Virology 213:590-599(1995).
 DR EMBL: U34966; AAC34629.1; -
 DR HSSP: P10889; IM12.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12; Chemokine_sm11.
 DR InterPro: IPR004827; TFC2IP.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCKC.
 DR SMART: SM00338; BRLZ; 1.
 DR SMART: SM00199; SCY; 1.
 FT NON_TER 1
 SQ SEQUENCE 203 AA; 23132 MW; DE42FE2A1C1A71C8 CRC64;
 Query Match 23.1%; Score 83; DB 12; Length 203;
 Best Local Similarity 23.5%; Pred. No. 0.02; Mismatches 13; Indels 32; Gaps 4;
 Matches 19; Conservative 17; Mismatches 13; Indels 32; Gaps 4;
 QY 1 KGVSLSYRCPCREFESHVARANVHKLILNTP-----NC-ALQIVARLK 43
 DB 95 ESLAVDKRC-----VKVTRNPTGLGPIIADVPIPGIHRRTETI 140
 QY 44 NNRNRCVCPREFESHVARANVHKLILNTP-----PNCALQIVARLK 58
 DB 141 KNRKVCVDEAPVWQOFIRK 160
 RESULT 11
 ID 090YD7 PRELIMINARY; PRT; 148 AA.
 AC 090YD7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Small inducible cytokine A2.
 GN SCY42.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-SJL/J; TISSUE=SPLEEN;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Sclay (TCA-3), Sclay2
 RT (monocyte chemoattractant protein (MCP)-1), and Sclay12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266(1999).
 DR EMBL: AF065929; SCLY1379.1; -;
 DR HSSP: P13500; 1DOK.
 DR MGD: MGI:98259; Sclay2.
 DR InterPro: IPR000827; CC_chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489EB CRC64;

Query Match 22.3%; Score 80; DB 11; Length 148;
 Best Local Similarity 24.6%; Pred. No. 0.034;
 Matches 15; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

OY 3 VSLSYRCRFESHVARANVKKHLILNTPNCALQIVARLKNRRQVCIIDPKLWIOEYL 62
 DB 28 VNAPLTCCSFSTSKMIPMSRLEGYKRITSSRCPEKAVVFVTKLREVCADPKKEWQYTI 87
 OY 63 E 63
 DB 88 K 88

RESULT 12
 OY3442 PRELIMINARY; PRT; 101 AA.
 ID O93442;
 AC O93442;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE LFCA-1 protein precursor.
 OS Lampetra fluviatilis (River lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxId=7748;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEUCOCYTES;
 RA Na)kshin A.M., Mechetina L.V., Alabyev B.Y., Taranin A.V.;
 RT "Identification of the interleukin 8 homologue of chemokines";
 RT fluviatilis): early evolutionary divergence of chemokines";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBD databases.
 DR EMBL: AJ231072; CAA13114.1; -;
 DR HSSP: P02775; 1TVX.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXC_chemkine_sml.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKXC.
 DR SMART: SM00199; SCY; 1.
 DR SIGNAL.
 KW SIGNAL.
 FT CHAIN 1 22 POTENTIAL.
 FT CHAIN 23 101 LFCA-1 PROTEIN.
 SQ SEQUENCE 101 AA; 11095 MW; 80CFEBE1EA7336D2 CRC64;

Query Match 22.1%; Score 79.5; DB 13; Length 101;
 Best Local Similarity 26.9%; Pred. No. 0.027;
 Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;

OY 8 RCRCRFESHVARANV--KHLK----ILNTPNCA-LQIVARLKNRRQVCIIDPKLWIOE 60
 DB 30 RCRC----VAVISKFTHPKHFOYMEVIPPSSNCKNVELITVTKSTNNQICLNDADAVRK 85
 OY 61 YLEKALN 67

DB 86 VISHILD 92

RESULT 13
 OY28724 PRELIMINARY; PRT; 108 AA.
 ID O28724;
 AC O28724;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1999 (TREMBlrel. 11, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE GRO (Permeability factor 2).
 GN RPF2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE;
 RA Yoshimura T., Modi W.S.;
 RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC
 RT chemokine subfamily in mammals.";
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 43-108 FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE;
 RX MEDLINE=95129889; PubMed=7828903;
 RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
 RA Martin T.R.;
 RT "Cloning of two rabbit GRO homologues and their expression in alveolar
 RT macrophages";
 RL Gene 151:337-338(1994).
 DR EMBL: U95808; AAB93924.1; -;
 DR EMBL: L28933; AAB66975.1; -;
 DR HSSP: P19875; 1ONK.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXC_chemkine_sml.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match 22.1%; Score 79.5; DB 6; Length 108;
 Best Local Similarity 27.4%; Pred. No. 0.029;
 Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

OY 8 RCRCRFESHVARANVKKHLILNTPNCA-LQIVARLKNRRQVCIIDPKLWIOEYLEKA 65
 DB 43 RCOCLOTVOGIIHLKSIQSLKVLSPGHCAOTEVIALTK-SGQACINPAAPVKKFLQKR 101
 OY 66 LN 67
 DB 102 LS 103

RESULT 14
 OY98702 PRELIMINARY; PRT; 97 AA.
 ID O98702;
 AC O98702;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative Interleukin 8 (Putative cxc chemokine precursor).
 GN IL-8.
 OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Onchorynchus.
 OX NCBI_TaxId=8022;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;
RT "Identification and analysis of the interleukin 8 molecule in rainbow
RL trout Oncorhynchus mykiss.";
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA Sangrador-Vegas A., Smith T.J.;
RT "Molecular cloning of a rainbow trout (Oncorhynchus mykiss) CX
RL chemokine by use of suppression subtractive hybridization.";
RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;
RT "Identification and analysis of the interleukin 8 molecule in rainbow
RL trout Oncorhynchus mykiss.";
RN Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ279069; CAC33585.1; -.
DR EMBL; AJ300835; CAC45061.1; -.
DR EMBL; AJ310565; CAC83945.1; -.
DR HSSP; P19875; 10NK.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXK_chukline_sml.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR SMART; SM00199; SCY; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 97 AA: 10777 MW: 4EBB35A4EF9DACE2 CRC64;

Query Match 22.0%; Score 79; DB 13; Length 97;
Best Local Similarity 25.0%; Pred. No. 0.03;
Matches 17; Conservative 18; Mismatches 31; Indels 2; Gaps 2;

OY 1 KGVSLSTYRCPCRFESHVARNVKKHLKLT-NTPNCA-LQIVARLKNNROYCIDPKLKI 58
Db 26 RGMGADLCRCIEETESRRIGRLIKVEMFPSPSHCRDEITATLSKSGEICLDVSA PW 85

OY 59 OEYLEKAL 66
Db 86 KRVIKML 93

RESULT 15
O92318 PRELIMINARY; PRT; 97 AA.
ID 092318;
AC O92318;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Monocyte chemoattractant protein-3 (MCP-3).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,
RA Ishizaka A., Yamaguchi K., Kanazawa M.;
RT "Differential expression of CC chemokines in guinea pig lungs during
RT an allergic inflammation.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014340; BAA36456.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA: 11159 MW: E1B9A17C165C2421 CRC64;

```

```

Query Match 21.9%; Score 78.5; DB 11; Length 97;
Best Local Similarity 30.3%; Pred. No. 0.034;
Matches 20; Conservative 13; Mismatches 28; Indels 5; Gaps 2;

OY 2 KGVSLSTYRCPCRFESHVARNVKKHLKLTNPNCALQIVARLKNNROYCIDPKLKI OE- 60
Db 27 GVNISTCCYKRSRIRVQR--LESYTRITSSKCPMAVIFKTKFNREICADPKQOOWQDS 84

OY 61 --YLEK 64
Db 85 MKYIDK 90

```

Search completed: January 23, 2003, 15:36:19
 job time : 24.6 secs

PA	(CHEM-)CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Tudan CR, Mezrouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
DR	WPI: 2002-106073/14.
XX	
PT	Promoting the rate of haematopoietic cell multiplication for treating a
PT	cancer involves administering chemokine receptor antagonist to the
PT	cells
XX	
PS	Claim 9, Page 54, 68pp; English.
XX	
CC	The invention relates to a method of promoting the rate of haematopoietic
CC	cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC	antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC	has cytosstatic and immunosuppressive activity and is useful for treating
CC	cancer or autoimmune disease in a patient; to promote the rate of
CC	haematopoietic cell multiplication; to formulate a medicament for
CC	increasing the circulation of the haematopoietic cells in a patient; for
CC	mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC	locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC	CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC	self-renewal, expansion and proliferation of peripheralisation in vivo.
XX	
SQ	Sequence 67 AA:
Query Match	100.0%; Score 362; DB 23; Length 67;
Best Local Similarity	100.0%; Pred. No. 1,9e-40;
Matches	67; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 KGVSPSYRCPGRFFESHVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
DB	1 KGVSPSYRCPGRFFESHVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
OY	61 YLEKALN 67
DB	61 YLEKALN 67
RESULT 2	
AAM48656	
ID	AAM48656 standard; peptide: 67 AA.
XX	
AC	AAM48656;
XX	
DT	20-MAY-2002 (first entry)
XX	
DE	CXCR4 peptide antagonist SEQ ID NO 1.
XX	
KW	CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;
KW	Immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW	cell multiplication.
XX	
SS	Synthetic.
XX	
PN	WO200185196-A2.
XX	
PD	15-NOV-2001.
XX	
PF	09-MAY-2001; 2001WO-CA00659.
XX	
PR	09-MAY-2000; 2000CA-2305787.
PR	19-MAY-2000; 2000US-205467P.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Tudan CR, Mezrouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
XX	WPI: 2002-106073/14.

Pt	Promoting the rate of haematopoietic cell multiplication for treating a
Pt	cancer involves administering chemokine receptor antagonist to the
Pt	cells -
PS	Claim 9; Page 54; 68pp; English.
XX	
XX	The invention relates to a method of promoting the rate of haematopoietic
CC	cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC	antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC	has cyostatic and immunosuppressive activity and is useful for treating
CC	cancer or autolimmune disease in a patient; to promote the rate of
CC	haematopoietic cell multiplication; to formulate a medicament for
CC	increasing the circulation of the haematopoietic cells in a patient; for
CC	mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC	locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC	CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC	self-renewal, expansion and proliferation of peripherallisation in vivo.
XX	
SQ	Sequence 67 AA:
	Query Match 97.2%; Score 352; DB 23; Length 67;
	Best Local Similarity 98.5%; Pred. No. 4e-39;
Matches	66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 KGVSESYRCPCRFESHVARANVKHLKILTPNCALQIVARLKNRRVOCIDPKLKWIOE 60 Db 1 KGVSLSYRCPCFEFESHVARANVKHLKITLPNCALQIVARLKNRRNROVCIDPKLKWIOE 60
Oy	61 YLEKALN 67 Db 61 YLEKALN 67
RESULT 3	
AAM48658	
ID	AAM48658 standard; peptide: 67 AA.
AC	AAM48658;
XX	
DT	20-MAY-2002 (first entry)
XX	
DE	CXCRA peptide antagonist SEQ ID NO 3.
XX	
KM	CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;
KW	Immunosuppressive; cancer; autolimmune disease; peripheral blood locus;
KW	cell multiplication.
XX	
OS	Synthetic.
XX	
PH	Key Location/Qualifiers
FT	Modified-site 6 /note= "Optionally the proline analogue 6-amino-7-oxo-2,
FT	3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
FT	acid residue or a bicyclic turned dipeptide
FT	(Brd)"
XX	
PN	WO200185196-A2.
XX	
PD	15-NOV-2001.
XX	
PF	09-MAY-2001; 2001WO-CA00659.
XX	
PR	09-MAY-2000; 2000CA-2305787.
PR	19-MAY-2000; 2000US-205467P.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMKINE THERAPEUTICS CORP.
XX	
PI	Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
OR	WPI; 2002-106073/14.
XX	

PT Promoting the rate of haematopoietic cell multiplication for treating a
PT cancer involves administering chemokine receptor antagonist to the
PT cells -
XX
XX Claim 9; Page 54; 68pp; English.
PS
XX
XX The invention relates to a method of promoting the rate of haematopoietic
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC has cytostatic and immunosuppressive activity and is useful for treating
CC cancer or autoimmune disease in a patient; to promote the rate of
CC haematopoietic cell multiplication; to formulate a medicament for
CC increasing the circulation of the haematopoietic cells in a patient; for
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC self-renewal, expansion and proliferation of peripheralisation in vivo.
XX
XX
SQ Sequence 67 AA:

Query Match 95.9%; Score 347; DB 23; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.9e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
DB 1 KGVSLPYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 4
AAM48660
ID AAM48660 standard; peptide: 67 AA.
XX
XX AAM48660;
AC
XX 20-MAY-2002 (first entry)
DT
XX
XX CXCR4 peptide antagonist SEQ ID NO 5.
DE
XX
XX CRCK4: haematopoietic cell; chemokine receptor-4; cytostatic;
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW cell multiplication.
XX
XX Synthetic.
OS
XX
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "Optionally the proline analogue 6-amino-7-oxo-2,
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
FT acid residue"
XX
XX
XX MO200185196-A2.
XX
XX
XX 15-NOV-2001.
PD
XX
XX 09-MAY-2001; 2001MO-CA00659.
PF
XX
XX 09-MAY-2000; 2000CA-2305787.
PR
XX 19-MAY-2000; 2000US-205467P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
XX Tuden CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI Clark-Lewis I, Salari H;
XX
XX WPI: 2002-106073/14.
DR
XX
XX Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the
PT cells -
XX
XX Claim 9; Page 54; 68pp; English.
PS
XX
XX The invention relates to a method of promoting the rate of haematopoietic
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC has cytostatic and immunosuppressive activity and is useful for treating
CC cancer or autoimmune disease in a patient; to promote the rate of
CC haematopoietic cell multiplication; to formulate a medicament for
CC increasing the circulation of the haematopoietic cells in a patient; for
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC self-renewal, expansion and proliferation of peripheralisation in vivo.
XX
XX
SQ Sequence 67 AA:

Query Match 95.3%; Score 345; DB 23; Length 67;
Best Local Similarity 97.0%; Pred. No. 3.4e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
DB 1 KGVSLPYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 5
AAM50760
ID AAM50760 standard; peptide: 67 AA.
XX
XX AAM50760;
AC
XX 27-JUL-1998 (first entry)
DT
XX
XX Peptide which binds to CXCR4 receptor and is useful for treating HIV.
DE
XX
XX Stromal cell-derived chemokine: SDF-1; human immunodeficiency virus;
KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
KW
XX
XX Homo sapiens.
OS
XX
XX FR2751658-A1.
PN
XX
XX 30-JAN-1998.
PD
XX
XX 26-JUL-1996; 96FR-0009477.
PF
XX
XX 26-JUL-1996; 96FR-0009477.
PR
XX
XX (INSP) INST PASTEUR.
PA
XX
XX Arenzana SF, Baggiolini M, Clark LJ, Moser B, Virelizier JL;
PI WPI: 1998-123039/12.
XX
XX Human stromal cell-derived chemokine, SDF-1 - useful for treating
PT human immunodeficiency virus infection
XX
XX
XX Claim 2; Page 29; 48pp; French.
PS
XX
XX The invention relates to peptides which bind to a cellular receptor for
CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC expressed transmembrane domain receptor), especially where the
CC peptide is human chemokine SDF-1. The peptide can be used to treat or
CC prevent HIV infections, optionally together with reverse transcriptase
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
CC receptor antagonists, immunotherapy agents, agents for treating HIV-

CC associated opportunistic infections and/or other CXC or CC chemokines,
 CC especially RANTES, MIP1- alpha, MIP1- beta or MCP1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.

XX
 SQ Sequence 67 AA;

Query Match 95.0%; Score 344; DB 19; Length 67;
 Best Local Similarity 97.0%; Pred. No. 4.7e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
 DB 1 KPVLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 6
 AAY34092
 ID AAY34092 standard; protein; 67 AA.

AC AAY34092;
 XX
 DT 29-NOV-1999 (first entry)

DE Native stromal cell derived factor 1 (SDF-1) alpha protein.

XX CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KW angiogenesis; stromal cell derived factor 1; SDF-1.

XX Mammalia.

XX WO9947158-A2.

XX 23-SEP-1999.

XX 12-MAR-1999; 99WO-CA00221.

XX 13-MAR-1998; 98CA-2226391.

XX 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Durotojo V;

XX WPI; 1999-561857/47.

XX Use of CXC chemokine receptor 4 for treating autoimmune disease and
 PT cancer

XX Example 1; Fig 1; 71pp; English.

XX The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)
 CC antagonist for the manufacture of a medicament for reducing interferon
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
 CC to treat or to design a medicament to treat, an autoimmune disease,
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
 CC antagonists may be peptide compounds comprising a substantially purified
 CC peptide fragment, analogue or a pharmacologically acceptable salt of
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents
 CC the amino acid sequence of SDF-1 alpha protein.

XX Sequence 67 AA;

Query Match 95.0%; Score 344; DB 20; Length 67;
 Best Local Similarity 97.0%; Pred. No. 4.7e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
 DB 1 KPVLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 7
 AAY06741
 ID AAY06741 standard; protein; 67 AA.

AC AAY06741;

DT 18-JUN-1999 (first entry)

DE SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
 KW infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;
 KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;
 KW stromal cell derived factor 1; Macrophage Inflammatory protein.

XX Synthetic.
 OS Homo sapiens.

XX WO9911655-A1.

XX 11-MAR-1999.

XX 31-AUG-1998; 98WO-US18096.

XX 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

XX Kent SBH, Siani MA, Simon R, Wilken J;

XX WPI; 1999-205128/17.

XX New cross-over proteins for treatment of inflammation and infections
 PT e.g. AIDS - prepared by ligation of two functional protein modules
 PT derived from two different parent molecules

XX Example 4; Page 43; 75pp; English.

XX The invention relates to a cross-over protein produced by chemical
 CC ligation of at least two functional protein modules derived from at
 CC least two parent protein molecules. The cross-over proteins can be used
 CC in pharmaceutical compositions for therapy of inflammatory and
 CC infectious diseases including AIDS, and for indications of hematopoiesis
 CC and chemoprotection. They are also useful for treatment of asthma,
 CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library
 CC comprising a collection of cross-over proteins is useful for screening
 CC for cross-over proteins that are receptor ligands. The libraries
 CC comprise functionally diverse compounds therefore improving the drug
 CC discovery process. The proteins and libraries are exemplified by the
 CC preparation of cross-over chemokines comprising various combinations of
 CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor
 CC 1), VMP (viral Macrophage Inflammatory protein) and other such
 CC chemokines. Sequences AAY06741-62 represent amino acid sequences of SDF-1
 CC alpha/RANTES cross-over molecules.

XX Sequence 67 AA;

Query Match 95.0%; Score 344; DB 20; Length 67;
 Best Local Similarity 97.0%; Pred. No. 4.7e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
 DB 1 KPVLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 8

AAV06726
 ID AAV06726 standard; protein; 67 AA.

XX AAV06726;

DT 18-JUN-1999 (first entry)

XX Amino acid fragment of SDF-1 alpha.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
 KW infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMIPI;
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;
 KM stromal cell derived factor 1; Macrophage Inflammatory protein.

OS Homo sapiens.
 OS Synthetic.

PN WO9911655-A1.

XX 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

PI Kent SBH, Slani MA, Simon R, Wilken J;

DR WPI: 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections
 PT e.g. AIDS - prepared by ligation of two functional protein molecules
 PT derived from two different parent molecules

PS Example 4; Page 41; 75pp; English.

XX The invention relates to a cross-over protein produced by chemical
 CC ligation of at least two functional protein modules derived from at least
 CC two parent protein molecules. The cross-over proteins can be used in
 CC pharmaceutical compositions for therapy of inflammatory and infectious
 CC diseases including AIDS, and for indications of hematopoiesis and
 CC chemoprotection. They are also useful for treatment of asthma, allergic
 CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library
 CC comprising a collection of cross-over proteins is useful for screening
 CC for cross-over proteins that are receptor ligands. The libraries comprise
 CC functionally diverse compounds therefore improving the drug discovery
 CC process. The proteins and libraries are exemplified by the preparation
 CC of cross-over chemokines comprising various combinations of peptide
 CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMIPI
 CC (viral Macrophage Inflammatory protein) and other such chemokines. The
 CC present sequence represents an amino acid fragment of SDF-1 alpha which
 CC acts as a synthetic base molecule for synthesizing the cross-over
 CC protein.

XX Sequence 67 AA:

Query Match 95.0%; Score 344; DB 20; Length 67;

Best Local Similarity 97.0%; Pred. No. 4.7e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLWIOE 60
 OY 61 YLEKALN 67

DB 61 YLEKALN 67

RESULT 9

AAV67594
 ID AAV67594 standard; peptide; 67 AA.

XX AAV67594;

DT 13-JUN-2000 (first entry)

XX SDF-1alpha peptide sequence.

XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;
 KM stromal cell derived factor one; anti-inflammatory; immunomodulatory.

OS Unidentified.

PN WO200009152-A1.

XX 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI: 2000-224175/19.

PT Therapeutic composition containing CXCR4 antagonist, useful for
 PT treating autoimmune disease, especially multiple sclerosis and cancer

PS Disclosure; Fig 1; 88pp; English.

XX The invention provides a therapeutic composition containing an antagonist
 CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions
 CC are specifically used to reduce production of gamma-interferon by T
 CC cells, particularly for treating autoimmune disease, especially multiple
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
 CC colitis, gout, lupus and transplant rejection; to treat cancer by
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
 CC evaluate in vivo pharmacokinetics, or to determine disease progression
 CC and susceptibility, or as targeting agents for delivery of other
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
 CC derived factor one) peptide fragments, SDF-1 being the only known natural
 CC ligand for CXCR4. The present sequence represents a SDF-1alpha
 CC peptide sequence.

XX Sequence 67 AA:

Query Match 95.0%; Score 344; DB 21; Length 67;

Best Local Similarity 97.0%; Pred. No. 4.7e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 10
 AAB47680

ID AAB47680 standard; peptide: 67 AA.
XX
AC AAB47680;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1-alpha.
XX
KM Hematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KM autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Homo sapiens.
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation -
XX
PS Claim 8; Page 57; 74pp; English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 67 AA;

Query Match 95.0%; Score 344; DB 23; Length 67;
Best Local Similarity 97.0%; Pred. No. 4.7e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPTRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
DB 1 KPVSLSTYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67

XX
DT 27-JUL-1998 (first entry)
XX
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
XX
KM Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
KM HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
XX
OS Homo sapiens.
XX
PN FR2751658-A1.
XX
PD 30-JAN-1998.
XX
PF 26-JUL-1996; 96FR-0009477.
XX
PR 26-JUL-1996; 96FR-0009477.
XX
PA (INSP) INST PASTEUR.
XX
PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
XX
DR WPI; 1998-123039/12.
XX
PT Human stromal cell-derived chemokine, SDF-1 - useful for treating
PT human immunodeficiency virus infection
XX
PS Claim 5; Page 29; 48pp; French.
XX
CC The invention relates to peptides which bind to a cellular receptor for
CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC expressed transmembrane domain receptor), especially where the
CC peptide is human chemokine SDF-1. The peptide can be used to treat or
CC prevent HIV infections, optionally together with reverse transcriptase
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
CC receptor antagonists, immunotherapy agents, agents for treating HIV-
CC associated opportunistic infections and/or other CXC or CC chemokines,
CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP1. The peptide can be
CC used to detect anti-SDF-1 antibodies in biological fluids. This
CC sequence represents a specifically claimed peptide which binds to the
CC CXCR4 receptor.
XX
SQ Sequence 68 AA;

Query Match 95.0%; Score 344; DB 19; Length 68;
Best Local Similarity 97.0%; Pred. No. 4.7e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPTRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
DB 2 KPVSLSTYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 61
QY 61 YLEKALN 67
DB 62 YLEKALN 68

RESULT 12
AAV05818
ID AAV05818 standard; Protein: 69 AA.
XX
AC AAV05818;
XX
DT 02-AUG-1999 (first entry)
XX
DE N-terminal modified chemokine met-hSDF-1 alpha.
XX
KM Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hSDF-1 alpha;
KM human; protein engineering; amino-terminal modification; mutant;
KM HIV; infection; angiogenesis; autoimmune disease; inflammation;
KM antiangiogenic; antiinflammatory; immunosuppressive; therapy;
XX
XX vaccine.

OS Homo sapiens.
 OS Synthetic.
 PN WO9920759-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 21-OCT-1998; 98WO-US22282.
 XX
 PR 20-OCT-1998; 98US-0175713.
 PR 22-OCT-1997; 97US-0955826.
 PR 27-FEB-1998; 98WO-US04002.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
 PI Yang O;
 DR WPI: 1999-288307/24.
 DR N-PSDB: AAX25530.
 XX
 PT Modified chemokines useful for inhibiting or stimulating
 PT angiogenesis
 PS
 XX Claim 6c: Page 79; 85pp; English.
 XX
 CC The present sequence represents met-hsDF-1 alpha, i.e. human
 CC stromal cell derived growth factor-1 alpha having an added
 CC N-terminal methionine residue. DNA encoding met-hsDF-1 alpha (see
 CC AA255530) was produced by cloning an NdeI/XbaI-restricted hSDF-1
 CC alpha PCR product into the E. coli expression vector pAL781
 CC in-frame with an ATG codon. met-hsDF-1 alpha is an example of
 CC novel N-terminal modified chemokines (see AA05818-21) that have at
 CC least one Met residue, at least one aminoxy-pentane residue or at
 CC least one GroHEK peptide (see AA05822) covalently attached at the
 CC N-terminus. The N-terminal modified chemokines are useful for
 CC altering receptor function, inhibiting interactions between
 CC chemokine receptors and their ligands. They are used as research
 CC tools for identifying chemokine receptors, as vaccine adjuvants, as
 CC agents for the chemotactic recruitment of migratory cells, as agents
 CC for the stimulation or inhibition of angiogenesis, as agents against
 CC autoimmune diseases and inflammation, and as agents to inhibit the
 CC binding of HIV to certain receptors and the infection of
 CC susceptible cells by HIV. HIV infection is best treated with
 CC modified SDF-1 alpha and beta or MIP-1 alpha and beta.
 XX
 SQ Sequence 69 AA:
 Query Match 95.0%; Score 344; DB 20; Length 69;
 Best Local Similarity 97.0%; Pred. No. 4,8e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSPSYRCPCHFFESHVARANVKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 2 KVSLSYRCPCHFFESHVARANVKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61
 QY 61 YLEKALN 67
 DB 62 YLEKALN 68
 XX
 RESULT 13
 ID AAM50762 standard; peptide; 72 AA.
 XX
 AC AAM50762;
 XX
 DT 27-JUL-1998 (first entry)
 XX
 DE Peptide which binds to CXCR4 receptor, and is useful for treating HIV.
 XX
 KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.

XX
 OS Homo sapiens.
 XX
 PN FR2751658-A1.
 XX
 PD 30-JAN-1998.
 XX
 PF 26-JUL-1996; 96FR-0009477.
 XX
 PR 26-JUL-1996; 96FR-0009477.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
 PI WPI: 1998-123039/12.
 DR
 PT Human stromal cell-derived chemokine, SDF-1 - useful for treating
 PT human immunodeficiency virus infection
 XX
 PS Claim 5; Page 29; 48pp; French.
 XX
 CC The invention relates to peptides which bind to a cellular receptor for
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-
 CC expressed transmembrane domain receptor), especially where the
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or
 CC prevent HIV infections, optionally together with reverse transcriptase
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-
 CC associated opportunistic infections and/or other CXCR4 or CC chemokines,
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.
 XX
 SQ Sequence 72 AA:
 Query Match 95.0%; Score 344; DB 19; Length 72;
 Best Local Similarity 97.0%; Pred. No. 5,1e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSPSYRCPCHFFESHVARANVKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 1 KVSLSYRCPCHFFESHVARANVKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 QY 61 YLEKALN 67
 DB 61 YLEKALN 67
 XX
 RESULT 14
 ID AAY34093 standard; protein; 72 AA.
 XX
 AC AAY34093;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Native stromal cell derived factor 1 (SDF-1) beta protein.
 XX
 KW CXCR4 chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KW angiogenesis; stromal cell derived factor 1; SDF-1.
 XX
 OS Mammalia.
 XX
 PN WO9947158-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 12-MAR-1999; 99WO-CA00221.
 XX
 PR 13-MAR-1998; 98CA-2226391.

```

PR 14-AUG-1998; 98CA-2245224.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Clark-Lewis I, Gong J, Duronio V;
PI
XX WPI; 1999-561857/47.
XX
XX Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and
PT cancer -
XX
XX Example 1; Fig 1; 71pp; English.
XX
XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)
CC antagonist for the manufacture of a medicament for reducing interferon
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
CC to treat or to design a medicament to treat, an autoimmune disease,
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
CC antagonists may be peptide compounds comprising a substantially purified
CC peptide fragment, analogue or a pharmacologically acceptable salt of
CC stromal cell derived factor 1 (SDF-1). The present sequence represents
CC the amino acid sequence of SDF-1 beta protein.
XX
XX
SQ Sequence 72 AA;
XX
XX Query Match 95.0%; Score 344; DB 20; Length 72;
XX Best Local Similarity 97.0%; Pred. No. 5,1e-38;
XX Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 KGVSTSYRCPCCFFESHVARANVKHLKILNTNCALQIYARLKNNNROYCIDPKLKWIOE 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 1 KPVSTSYRCPCCFFESHVARANVKHLKILNTNCALQIYARLKNNNROYCIDPKLKWIOE 60
XX
XX 61 YLEKALN 67
XX | | | | |
XX 61 YLEKALN 67
XX
XX
XX RESULT 15
XX ID AAY67595
XX AAY67595 standard; peptide; 72 AA.
XX
XX AAY67595;
XX
XX 13-JUN-2000 (first entry)
XX
XX SDF-1beta peptide sequence.
XX
XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
XX autoimmune disease; multiple sclerosis; Rheumatoid arthritis; psoriasis;
XX type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;
XX stromal cell derived factor one; anti-inflammatory; immunomodulatory.
XX
XX Unidentified.
XX
XX WO200009152-A1.
XX
XX 24-FEB-2000.
XX
XX 16-AUG-1999; 99WO-CA00750.
XX
XX 14-AUG-1998; 98CA-2245224.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Clark-Lewis I, Gong J, Duronio V, Salari H;
XX
XX WPI; 2000-224175/19.
XX
XX Therapeutic composition containing CXCR4 antagonist, useful for
XX treating autoimmune disease, especially multiple sclerosis and cancer
XX

```

[illegible]

Search completed: January 23, 2003, 15:33:42
Job time : 29.2 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:33:47 : Search time 9.8 Seconds
(without alignments)
201.157 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362

Sequence: 1 KCVSPSYRCPCRFESHVAR.....QVCIDPKLKWIELEKALN 67

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents-AA:
1: /cgn2_6/pdata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/pdata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/pdata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/pdata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.0	89	1	US-08-323-084A-1
2	344	95.0	89	1	US-08-674-008-1
3	344	95.0	93	1	US-08-323-084A-5
4	344	95.0	93	1	US-08-674-008-5
5	344	95.0	326	3	US-08-808-720-3
6	344	95.0	328	3	US-08-808-720-1
7	343	94.8	89	1	US-08-181-556-2
8	94.5	26.1	70	1	US-08-330-163-24
9	94.5	26.1	70	1	US-08-482-111-24
10	94	26.0	67	1	US-08-244-702-12
11	94	26.0	67	1	US-08-244-702-14
12	94	26.0	68	1	US-08-244-702-9
13	94	26.0	68	1	US-08-244-702-10
14	94	26.0	68	1	US-08-244-702-11
15	94	26.0	68	1	US-08-244-702-12
16	94	26.0	69	1	US-08-244-702-8
17	94	26.0	72	1	US-07-956-863-1
18	94	26.0	72	1	US-07-778-413E-16
19	94	26.0	72	1	US-08-340-102-16
20	94	26.0	72	1	US-08-330-163-1
21	94	26.0	72	1	US-08-244-702-1
22	94	26.0	72	1	US-08-482-111-1
23	94	26.0	72	1	US-08-202-989-1
24	94	26.0	72	5	PCT-US94-02051-1
25	94	26.0	73	1	US-08-482-111-69
26	94	26.0	73	4	US-09-384-302A-26
27	94	26.0	76	2	US-08-468-819-79

28	94	26.0	76	2	US-08-468-819-81	Sequence 81, Appl
29	94	26.0	79	2	US-08-436-420-25	Sequence 25, Appl
30	94	26.0	99	1	US-08-352-324A-6	Sequence 6, Appl
31	94	26.0	99	2	US-08-862-607-6	Sequence 6, Appl
32	94	26.0	99	2	US-08-468-819-3	Sequence 3, Appl
33	94	26.0	99	3	US-09-203-235-6	Sequence 6, Appl
34	94	26.0	99	4	US-08-679-493A-150	Sequence 150, App
35	94	26.0	99	5	PCT-US95-16144-6	Sequence 6, Appl
36	94	26.0	99	6	5451399-2	Patent No. 5451399
37	92.5	25.6	72	3	US-08-846-966-1	Sequence 1, Appl
38	92.5	25.6	72	3	US-08-557-142-1	Sequence 1, Appl
39	92.5	25.6	72	4	US-09-467-160-1	Sequence 1, Appl
40	92.5	25.6	72	4	US-09-513-153-1	Sequence 1, Appl
41	92.5	25.6	72	4	US-09-467-155-1	Sequence 1, Appl
42	92.5	25.6	72	5	PCT-US94-06264-1	Sequence 1, Appl
43	92.5	25.6	77	2	US-08-436-420-41	Sequence 41, Appl
44	92	25.4	64	1	US-08-330-163-21	Sequence 21, Appl
45	92	25.4	64	1	US-08-482-111-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-323-084A-1
; Sequence 1, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; City: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-1
Query Match 95.0%; Score 344; DB 1; Length 89;
Best local Similarity 97.0%; Pred. No. 1.9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KCVSPSYRCPCRFESHVARANKHLKILNTPKCALQIVARLKNRRNROVVIDPKLKWIOE 60
DB 22 KCVSLSYRCPCRFESHVARANKHLKILNTPKCALQIVARLKNRRNROVVIDPKLKWIOE 81
QY 61 YLEKALN 67

Db 82 YLEKALN 88

RESULT 2

US-08-674-008-1
; Sequence 1, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-674-008-1

Query Match 95.0%; Score 344; DB 1; Length 89;
Best Local Similarity 97.0%; Pred. No. 1,9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVSFSTRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 22 KVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 3

US-08-323-084A-5
; Sequence 5, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-5

Query Match 95.0%; Score 344; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVSFSTRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 22 KVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 4

US-08-674-008-5
; Sequence 5, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; APPLICANT: TADA, Hideaki
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994

US-08-482-111-24

Query Match	26.18;	Score 94.5;	DB 1;	Length 70;
Best Local Similarity	32.88;	Pred. No. 3.2e-05;		
Matches 20; Conservative	17;	Mismatches 21;	Indels 3;	Gaps 3;

Oy 8 RCPREFEESHARANVKHLKILNT-PNC-ALQIVARKNNNOYCIDPKLWIGLEYLEKA 65

Dd 9 QCLCVKTTSOVRPHRTSLEVIAKGPHCPTAQLIATLK-NGRKLCDLPKENMVKKIIKKL 67

Qy	66	L	66
		1	
Db	68	L	68

```

: RESULT 10
: US-08-244-702-12
: Sequence 12, Application US/082444702
: Patent No. 5665346
: GENERAL INFORMATION:
: APPLICANT: Clark-Lewis, Ian
: APPLICANT: Moser, Bernhard
: TITLE OF INVENTION: Human Interleukin-8 Analogs
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/244,702
: FILING DATE: 27-SEP-1994
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/CA92/00528
: FILING DATE: 03-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/801,578
: FILING DATE: 04-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 8080-0004,20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 67 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: IS-08-244-702-12

```

	Query Match	26.0%	Score 94;	DB 1:	Length 67;	
	Best Local Similarity	32.3%	Pred. No. 3.5e-05;			
	Matches	20;	Conservative 18;	Mismatches 20;	Indels 4;	Gaps 4.
Oy	8 RCPG-RPFESHVARANVHKLILN ^T -PNC ^A -LQIYARLKNNROYCIDPKLWIOEYLEK	64				
	: : : : : : : : :					
Db	1 RCQCITYSKRPHPKFIEIKELRVIESGPCANTETIVKL-SDGRELCLDPKENMVORVEK	59				
Oy	65 AL 66					
Db	60 FL 61					

RESULT 11
US-08-244-702-14

Sequence 14, Application US/08244702
Patent No. 5655346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington

Query Match	26.08	Score	94	DB	1	Length	67
Best Local Similarity	32.38	Pred. NO.	3.5e-05				
Matches	20	Conservative	18	Mismatches	20	Indels	4
						Gaps	4

OY 8 RCPC-REFESHVARANVKILKILNT-PCNA-QQIYAARKNNRPOVCDPLTKIOEYLEK 64
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 4 RQCQIKKYNSFPHPKPIKELRVIESGSPHCANTEIIYKL-SGRRLCLDPRENNVOQRVYEK 62

OY 65 AL 66
|
Db 63 FL 64

RESULT 12
US-08-244-702-9
Sequence 9, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-9

Query Match 26.0%; Score 94; DB 1; Length 68;
Best Local Similarity 32.3%; Pred. No. 3.6e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVARANVHKILINT-PNCA-LOIVARLKNNNQVCIDPRKWIQYELK 64
DB 2 RQCICITYSKPHKPKIKELRVIESGPHCANTEIYKL-SDGRELCIDPRENNVQRYVEK 60
QY 65 AL 66
DB 61 FL 62

RESULT 13
US-08-244-702-10
Sequence 10, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578

FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-10

Query Match 26.0%; Score 94; DB 1; Length 68;
Best Local Similarity 32.3%; Pred. No. 3.6e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVARANVHKILINT-PNCA-LOIVARLKNNNQVCIDPRKWIQYELK 64
DB 2 RQCICITYSKPHKPKIKELRVIESGPHCANTEIYKL-SDGRELCIDPRENNVQRYVEK 60
QY 65 AL 66
DB 61 FL 62

RESULT 14
US-08-244-702-11
Sequence 11, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-11

Query Match	26.0%;	Score 94;	DB 1;	Length 68;
Best Local Similarity	32.3%;	Pred. NO. 3.6e-05;		
Matches 20; Conservative	18;	Mismatches 20;	Indels 4;	Gaps 4;

Oy 8 RCPC-RFEESHVARANVKKHLKILNT-PNCA-LQIVARLKNNRQVCIDPKLKWIDEYLEK 64
 || : : : || :: : || : : : || : : ||
Dd 2 RQCICKTYSKPFHPKFIELRVIESGPHCANTEIIVKL-SDGRCLCPKENMVQRVER 600

Qy	65 AL 66
	—
Db	61 FL 62

RESULT 15
US-08-244-702-2
; Sequence 2, Application US/08244702
; Patent No. 565346

```

GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
Type: amino acid
TOPOLOGY: linear
US-08-244-702-2

```

Query Match	26.0%;	Score 94;	DB 1;	Length 69;
Best Local Similarity	32.3%;	Pred. NO. 3.6e-05;		
Matches	20;	Conservative	18;	Mismatches 20;
			Indels	4;
			Gaps	4;

Oy 8 RCPC-RFEESHVARANKVHLKIINT-PNCA-LQIVARLKNNNROYCIDPKLKWIEYLEK 64
 || : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Dd 3 RCGCIKTYSKPFPFKFIELRLVIESGPHCANTEIILKL-SDGEELCLDPEKENWYGRVEK 61

QY	65	AL	66
		1	
Db	62	FL	63

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 ; Search time 6.2 Seconds

(without alignments)
218.059 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362
Sequence: 1 KGVSPSYRCPCRFESHVAR.....QVCIDPKLKIQETLEKALN 67

Scoring table:

BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCRT_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCRTUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	67	9	US-09-852-424-2
2	353	97.5	67	9	US-09-852-424-6
3	352	97.2	67	9	US-09-852-424-1
4	348	96.1	67	9	US-09-852-424-7
5	347	95.9	67	9	US-09-852-424-3
6	346	95.6	67	9	US-09-852-424-9
7	345	95.3	67	9	US-09-852-424-5
8	344	95.0	67	9	US-09-852-424-8
9	344	95.0	67	9	US-09-852-107-1
10	344	95.0	67	10	US-09-144-838-8
11	344	95.0	67	10	US-09-144-838-23
12	344	95.0	89	8	US-08-927-939-22
13	344	95.0	89	9	US-09-792-793A-32
14	344	95.0	89	10	US-09-953-692-4
15	344	95.0	89	10	US-09-953-717-4
16	344	95.0	93	8	US-08-927-939-56
17	344	95.0	93	9	US-09-835-107-2
18	344	95.0	93	9	US-09-835-107-3
19	344	95.0	93	9	US-09-792-793A-93

20	344	95.0	93	10	US-09-144-838-7	Sequence 7, Appl
21	344	95.0	93	10	US-09-919-497-95	Sequence 95, Appl
22	344	95.0	320	9	US-09-792-793A-77	Sequence 77, Appl
23	344	95.0	322	9	US-09-792-793A-78	Sequence 78, Appl
24	344	95.0	327	9	US-09-792-793A-79	Sequence 79, Appl
25	342	94.5	67	9	US-09-852-424-4	Sequence 4, Appl
26	340.5	94.1	66	9	US-09-852-424-10	Sequence 10, Appl
27	330.5	91.3	66	9	US-09-852-424-11	Sequence 11, Appl
28	328.5	90.7	66	9	US-09-852-424-12	Sequence 12, Appl
29	326.5	90.2	66	10	US-09-144-838-27	Sequence 27, Appl
30	320	88.4	68	10	US-09-144-838-31	Sequence 31, Appl
31	304	84.0	67	10	US-09-144-838-47	Sequence 47, Appl
32	293	80.9	68	10	US-09-144-838-24	Sequence 24, Appl
33	290	80.1	67	10	US-09-144-838-25	Sequence 25, Appl
34	275.5	76.1	67	10	US-09-144-838-28	Sequence 28, Appl
35	269	74.3	69	10	US-09-144-838-52	Sequence 52, Appl
36	266	73.5	68	10	US-09-144-838-53	Sequence 53, Appl
37	253	69.9	68	10	US-09-144-838-48	Sequence 48, Appl
38	252.5	69.8	66	10	US-09-144-838-29	Sequence 49, Appl
39	250	69.1	67	10	US-09-144-838-49	Sequence 26, Appl
40	239	66.0	68	10	US-09-144-838-26	Sequence 30, Appl
41	221.5	61.2	67	10	US-09-144-838-30	Sequence 31, Appl
42	221	61.0	67	10	US-09-144-838-31	Sequence 54, Appl
43	215	59.4	69	10	US-09-144-838-54	Sequence 35, Appl
44	210.5	58.1	66	10	US-09-144-838-35	Sequence 50, Appl
45	199	55.0	68	10	US-09-144-838-50	

ALIGNMENTS

RESULT 1
US-09-852-424-2
Sequence 2, Application US/09852424
Patent No. US20020156034A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia; and
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: 80021-257
CURRENT APPLICATION NUMBER: US/09/852,424
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: CA 2,305,787
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 60/205,467
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Engineered In
US-09-852-424-2
Query Match
Best Local Similarity 100.0%; Score 362; Length 67;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGVSPSYRCPCRFESHVARAVKHKILNTPCAQIYARLKNRROVCIDPKLWIDE 60
DB 1 KGVSPSYRCPCRFESHVARAVKHKILNTPCALQIVARLKNRROVCIDPKLWIDE 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67
RESULT 2
US-09-852-424-6
Sequence 6, Application US/09852424

; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (5)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-6

Query Match 97.5%; Score 353; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 1,4e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLXYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 3
US-09-852-424-1
; Sequence 1, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-1

Query Match 97.2%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 1,4e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLXYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 4
US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-7

Query Match 96.1%; Score 348; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 4e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLXYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 5
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory

US-09-852-424-3

Query Match 95.9%; Score 347; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 5.1e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 6
US-09-852-424-9
Sequence 9, Application US/09852424
Patent No. US20020156034A1

GENERAL INFORMATION:
APPLICANT: The University of British Columbia; and
APPLICANT: Chemokine Therapeutics Corporation
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: 80021-257
CURRENT APPLICATION NUMBER: US/09/852,424

PRIOR APPLICATION NUMBER: CA 2,305,787
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 60/205,467
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (8)
OTHER INFORMATION: xaa=p*-proline-amino acid chimera. See page 17 of
OTHER INFORMATION: disclosure for possible structures for p*
OTHER INFORMATION: Description of Artificial Sequence: Engineered in
OTHER INFORMATION: Laboratory
US-09-852-424-9

Query Match 95.6%; Score 346; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 6.6e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 7
US-09-852-424-5
Sequence 5, Application US/09852424
Patent No. US20020156034A1

GENERAL INFORMATION:
APPLICANT: The University of British Columbia; and
APPLICANT: Chemokine Therapeutics Corporation
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: 80021-257
CURRENT APPLICATION NUMBER: US/09/852,424

PRIOR APPLICATION NUMBER: CA 2,305,787
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 60/205,467
PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Engineered in
OTHER INFORMATION: Laboratory
US-09-852-424-5

Query Match 95.3%; Score 345; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 8.5e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 8
US-09-852-424-8
Sequence 8, Application US/09852424
Patent No. US20020156034A1

GENERAL INFORMATION:
APPLICANT: The University of British Columbia; and
APPLICANT: Chemokine Therapeutics Corporation
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: 80021-257
CURRENT APPLICATION NUMBER: US/09/852,424

PRIOR APPLICATION NUMBER: CA 2,305,787
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 60/205,467
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (7)
OTHER INFORMATION: xaa=p*-proline-amino acid chimera. See page 17 of
OTHER INFORMATION: disclosure for possible structures for p*
OTHER INFORMATION: Description of Artificial Sequence: Engineered in
OTHER INFORMATION: Laboratory
US-09-852-424-8

Query Match 95.0%; Score 344; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 9
US-09-835-107-1
Sequence 1, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudean, Christopher R.

APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: SDF-1 alpha
US-09-835-107-1

Query Match 95.0%; Score 344; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db 1 KPVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
RESULT 10
US-09-144-838-8
Sequence 8, Application US/09144838A
Patent No. US20020051996A1
GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GREN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 8
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8

Query Match 95.0%; Score 344; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db 1 KPVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67
Db 61 YLEKALN 67
RESULT 11
US-09-144-838-23
Sequence 23, Application US/09144838A
Patent No. US20020051996A1
GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GREN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 23
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-23

Query Match 95.0%; Score 344; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db 1 KPVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
RESULT 12
US-08-927-939-22
Sequence 22, Application US/08927939
Patent No. US20010006640A1
GENERAL INFORMATION:
APPLICANT: Gralinger, David J.
APPLICANT: Tatalick, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022US1
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-927-939-22

Query Match 95.0%; Score 344; DB 8; Length 89;
Best Local Similarity 97.0%; Pred. No. 1.4e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db 22 KPVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
Db 61 YLEKALN 67

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds
(Without alignments) 555.259 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362
Sequence: 1 KGVSPSYRCPCRFESHVAR.....OVCIDPKLKWIOEYLEKALN 67

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.0	93	2	G01540 cytokine SDF-1-bet
2	343	94.8	89	2	A53497 pre-B-cell growth-
3	343	94.8	89	2	I53416 Interleukin-8 homo
4	343	94.8	93	2	I81182 cytokine - mouse
5	101	27.9	101	2	I48148 Neutrophil attract
6	99	27.3	95	2	JN0841 Interleukin-8 - do
7	94	26.0	99	2	A37034 Interleukin-8 prec
8	93	25.7	101	2	S42496 Interleukin-8 prec
9	92.5	25.6	96	2	A53094 gro-alpha precurs
10	92	25.4	103	2	A53096 Interleukin-8 prec
11	90.5	25.0	91	1	A46539 monocyte chemoatr
12	89.5	24.7	96	2	JN0572 neutrophil chemo-a
13	88	24.3	101	2	I46871 Interleukin-8 - ra
14	88	24.3	120	2	I48147 monocyte chemoatr
15	86.5	23.9	100	2	JH0200 macrophage inflam
16	85.5	23.6	91	1	A28815 monocyte chemoatr
17	85	23.5	109	2	A54678 monocyte chemoatr
18	82.5	22.8	75	2	A54188 granulocyte chemot
19	81.5	22.5	75	2	B54188 granulocyte chemot
20	81.5	22.5	92	2	I52322 macrophage inflam
21	81.5	22.5	100	2	S21467 macrophage inflam
22	81.5	22.5	100	2	I55614 macrophage inflam
23	81.5	22.5	119	2	S42881 platelet basic pro
24	81.5	22.5	120	2	JE0177 lymphocyte and mon
25	81	22.4	148	1	A30209 PCGF-inducible JE
26	81	22.4	148	1	S07723 immediate-early se
27	79.5	22.0	101	2	B28414 GRO-gamma precurs
28	79.5	22.0	107	2	B38290 melanoma growth-st
29	79.5	22.0	107	2	A28414

30	78.5	21.7	132	2	A57325
31	77.5	21.4	114	2	A55010
32	77.5	21.4	117	2	B44253
33	76.5	21.1	103	2	A26736
34	76.5	21.1	103	2	I50417
35	74.5	20.6	96	2	I48099
36	73.5	20.3	107	2	JH0281
37	72.5	20.0	126	2	A35766
38	72.5	20.0	870	2	A41130
39	72	19.9	92	2	A32393
40	72	19.9	96	2	JC2478
41	71.5	19.8	128	1	TGHU
42	70.5	19.5	53	2	I64831
43	70.5	19.5	90	2	S69133
44	69.5	19.2	104	1	PFH04A
45	69	19.1	93	2	B35673

ALIGNMENTS

RESULT 1

G01540

Cytokine SDF-1-beta - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999

C:Accession: G01540

R:Spotila, L.D.
submitted to the EMBL Data Library, October 1994

A:Reference number: G07697

A:Accession: G01540

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-93 <SPO>

A:Cross-references: EMBL:U16752; NID:91272194; PID:9571508

C:Superfamily: beta-thromboglobulin

Query Match

Best Local Similarity 95.0%: Score 344; DB 2; Length 93;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy	1	KGVSPSYRCPCRFESHVARANKHLKILNPNCAIQIYARLKNNNROYCIDPKLKWIOE 60
Db	22	KPVSLSTPCPCRFESHVARANKHLKILNPNCAIQIYARLKNNNROYCIDPKLKWIOE 81
Oy	61	VLEKALN 67
Db	82	VLEKALN 88

RESULT 2

A53497

pre-B-cell growth-stimulating factor precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000

C:Accession: A53497; I59582

R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994

A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.

A:Reference number: A53497; MUID:94181581; PMID:8134392

A:Accession: A53497

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-89 <NAG>

A:Cross-references: GB:D21072; NID:9413905; PIDN:BA04648.1; PID:9468457

R:Tashiro, K.; Tada, H.; Helliker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993

A:Title: Signal sequence tripp: a cloning strategy for secreted proteins and type I me

A:Reference number: I59582; MUID:93342488; PMID:8342023

A:Accession: I59582

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: GB:L12029; NID:g9393179; PIDN:AAA40100.1; PID:g9393180
 C:Genetics:
 A:Gene: SDF-1-alpha
 C:Superfamily: beta-thromboglobulin
 C:Keywords: cytokine

Query Match 94.8%; Score 343; DB 2; Length 89;
 Best Local Similarity 95.5%; Pred. No. 3.5e-35;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKIINTPCALQIIVARLKNNNROYCIDPKLKWIOE 60
 DB 22 KPVSLSYRCPCRFESHIRAVANKHLKIINTPCALQIIVARLKNNNROYCIDPKLKWIOE 81
 OY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 3

Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I53416
 R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
 Exp. Cell Res. 215, 284-293, 1994
 A:Title: Molecular cloning of TPRL1, a gene whose expression is repressed by the tumor F

A:Accession: I53416
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-89 <RES>
 A:Cross-references: GB:S74318; NID:g786393; PIDN:AAB32650.1; PID:g786394
 C:Genetics:
 A:Gene: TPRL1
 C:Superfamily: beta-thromboglobulin

Query Match 94.8%; Score 343; DB 2; Length 89;
 Best Local Similarity 95.5%; Pred. No. 3.5e-35;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKIINTPCALQIIVARLKNNNROYCIDPKLKWIOE 60
 DB 22 KPVSLSYRCPCRFESHIRAVANKHLKIINTPCALQIIVARLKNNNROYCIDPKLKWIOE 81
 OY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 4

Interleukin-8 homolog - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I81182
 R:Tashiro, K.; Tada, H.; Heliker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
 Science 261, 600-603, 1993
 A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr
 A:Reference number: 159582; MUID:93342488; PMID:8342023
 A:Accession: I81182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-93 <RES>
 A:Cross-references: GB:L12030; NID:g9393181; PIDN:AAA40101.1; PID:g9393182
 C:Genetics:
 A:Gene: SDF-1-beta
 C:Superfamily: beta-thromboglobulin

Query Match 94.8%; Score 343; DB 2; Length 93;
 Best Local Similarity 95.5%; Pred. No. 3.6e-35;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKIINTPCALQIIVARLKNNNROYCIDPKLKWIOE 60
 DB 22 KPVSLSYRCPCRFESHIRAVANKHLKIINTPCALQIIVARLKNNNROYCIDPKLKWIOE 81

OY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 5

Neutrophil attractant protein-1 - guinea pig

C:Species: Cavia porcellus (guinea pig)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
 C:Accession: I48148
 R:Yoshimura, T.; Johnson, D.G.
 J. Immunol. 151, 6225-6236, 1993
 A:Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (N
 A:Reference number: I48148; MUID:94065176; PMID:7504015
 A:Accession: I48148
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-101 <RES>
 A:Cross-references: GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765
 C:Genetics:
 A:Gene: NAP-1
 C:Superfamily: beta-thromboglobulin

Query Match 27.9%; Score 101; DB 2; Length 101;
 Best Local Similarity 35.9%; Pred. No. 3.1e-05;
 Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

OY 8 RCPGRFESHVARAN--VKHLKIINT-PCNA-LQIVARLKNNNROYCIDPKLKWIOEYL 62
 DB 33 RCQC--IKHTTPHFKFKELKVLKESGPCANSEITVRL-SNKRQLCDPKKKWYQDVV 89

OY 63 EKAL 66
 DB 90 SMFL 93

RESULT 6

Interleukin-8 - dog

C:Species: Canis lupus familiaris (dog)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995
 C:Accession: JN0841
 R:Shikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
 Gene 131, 305-306, 1993
 A:Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene
 A:Reference number: JN0841; MUID:94010328; PMID:7916715
 A:Accession: JN0841
 A:Molecule type: DNA
 A:Residues: 1-95 <ISH>
 C:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is 1
 C:Genetics:
 A:Introns: 22/1; 67/2
 C:Superfamily: beta-thromboglobulin

Query Match 27.3%; Score 99; DB 2; Length 95;
 Best Local Similarity 34.8%; Pred. No. 5.1e-05;
 Matches 23; Conservative 15; Mismatches 20; Indels 8; Gaps 4;

OY 3 VSPSYRCPCRFESHVARANKHLKIINT-PCNA-LQIVARLKNNNROYCIDPKLKW 57
 DB 28 VSELRCQC--IKHTSTPHPKYIKELRVIDSGPHCENSEIIVKLENGN-EVCLDPKEKW 84

OY 58 IOEYLE 63
 DB 85 VOKVVO 90

A:Molecule type: mRNA
 A:Residues: 1-99 <RE2>
 A:Cross-references: GB:M17017; NID:9179579; PIDN:AAA35611.1; PID:9179580
 R:Kusner, D.J.; Luebers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J.
 Kidney Int. 39, 1240-1248, 1991
 A:Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells
 A:Reference number: 137902; MUID:91374977; PMID:1895676
 A:Accession: 137902
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-97 <RE3>
 A:Cross-references: EMBL:Z11686; NID:933956; PIDN:CAA77745.1; PID:933959
 R:Alouani, S.; Gaertner, H.F.; Wermud, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; Pi
 Eur. J. Biochem. 227, 328-334, 1995
 A:Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at t
 A:Reference number: S67519; MUID:95154308; PMID:7851404
 A:Accession: S67519
 A:Molecule type: mRNA
 A:Residues: 1-99 <ALO>
 C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
 C:Comment: This protein is variably processed at the amino end. The major form differs
 C:Genetics:
 A:Gene: GDB:IL8
 A:Cross-references: GDB:120099; OMIM:146930
 A:Map position: 4q13-4q21
 A:Introns: 22/1; 67/2; 95/2
 C:Superfamily: beta-thromboglobulin
 C:Keywords: chemotaxis; cytokine; inflammation
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-99/Product: interleukin-8, minor form #status experimental <MAT>
 F:23-99/Product: interleukin-8, major lymphocyte-monocyte-derived form #status experimen
 F:28-99/Product: interleukin-8, major lymphocyte-monocyte-derived form #status experimen

Query Match 26.0%; Score 94; DB 2; Length 99;
 Best Local Similarity 32.3%; Pred. No. 0.00022;
 Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

Qy 8 RCPCRFESHVARANKHLKILNT-PNCA-LQIVARLKNNNRQVCIDPKLKWIOEYLEK 64
 Db 33 RCQCITRYSRPHKPKIKELRVIESGPHCANETIIVKL-SDGRCLDLPENNVQRYVEK 91

Qy 65 AL 66
 Db 92 FL 93

RESULT 8
 S42496
 Interleukin-8 precursor [similarity] - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-Jan-2001
 C:Accession: S42496; I46997
 R:Legssteleis, I.; Greenland, T.; Arnaud, P.; Morneix, J.F.; Cordier, G.
 submitted to the EMBL Data Library, March 1994
 A:Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain re
 A:Reference number: S42496
 A:Accession: S42496
 A:Molecule type: mRNA
 A:Residues: 1-101 <LEG>
 A:Cross-references: EMBL:X78306; NID:9463253; PIDN:CAA55115.1; PID:9463254
 R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
 Immunol. Cell Biol. 72, 398-405, 1994
 A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte
 A:Reference number: I46997; MUID:95137661; PMID:7835984
 A:Accession: I46997
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-101 <SEO>
 A:Cross-references: GB:S74436; NID:9786590; PIDN:AA833241.1; PID:9786591
 A:Gene: IL-8
 C:Superfamily: beta-thromboglobulin
 C:Keywords: chemotaxis; cytokine; inflammation

F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-101/Product: interleukin-8 #status predicted <MAT>

Query Match 25.7%; Score 93; DB 2; Length 101;
 Best Local Similarity 30.4%; Pred. No. 0.0003;
 Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

Qy 3 VSPSYRCPGRFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNNRQVCIDPKLKW 57
 Db 28 MSRELRCQC--IKTSTPPHPRKIKELRVIESGPHCANETIIVKL-TNCKEVCIDPKKRW 84

Qy 58 IDEYLEKAL 66
 Db 85 VQKVOAFL 93

RESULT 9
 A32954
 gro-alpha precursor - mouse
 N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1999
 C:Accession: A32954; JH0081
 R:Quenod, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
 J. Biol. Chem. 264, 4133-4137, 1989
 A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro
 A:Reference number: A32954; MUID:89139485; PMID:2917992
 A:Accession: A32954
 A:Molecule type: mRNA
 A:Residues: 1-96 <QOU>
 A:Cross-references: GB:J04596; NID:9201042; PIDN:AAA40131.1; PID:9201043
 R:Ryssek, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
 Exp. Cell Res. 180, 266-275, 1989
 A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou
 A:Reference number: JH0081; MUID:89078502; PMID:2909392
 A:Accession: JH0081
 A:Molecule type: mRNA
 A:Residues: 1-96 <RYS>
 C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
 C:Genetics:
 A:Map position: 5
 C:Superfamily: beta-thromboglobulin
 C:Keywords: extracellular protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-96/Product: gro-alpha #status predicted <MAT>

Query Match 25.6%; Score 92.5; DB 2; Length 96;
 Best Local Similarity 30.3%; Pred. No. 0.00033;
 Matches 20; Conservative 19; Mismatches 24; Indels 3; Gaps 3;

Qy 3 VSPSYRCPGRFESHVARANKHLKIL-NTPNCA-LQIVARLKNNNRQVCIDPKLKWIOE 60
 Db 27 IANELRCQCQLQTMAGHILKNIGSLKVLPSGPHCTQREVIATLTK-NGRKACLDPEAPLVQK 85

Qy 61 YLEKAL 66
 Db 86 IVQKML 91

RESULT 10
 A53096
 Interleukin-8 precursor - pig
 N:Alternate names: alveolar macrophage chemotactic factor-I (MwCF-I)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Jan-2001
 C:Accession: A53096; A44253
 R:Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta
 J. Biol. Chem. 269, 77-85, 1994
 A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba
 A:Reference number: A53096; MUID:94103307; PMID:8276881
 A:Accession: A53096
 A:Status: preliminary
 A:Molecule type: mRNA

A:Accession: S51214
 A:Molecule type: protein
 A:Residues: 25-96 <HAN>
 C:Comment: This protein has chemotactic activity for neutrophils and has melanoma growth C:Genetics:
 A:Gene: gro; KC
 A:introns: 24/1; 65/2; 92/2
 C:Superfamily: beta-thromboglobulin
 C:Keywords: cytokine; signal sequence #status predicted <SIG>
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-96/Product: neutrophil chemo-attractant gro protein #status experimental <CYT>

Query Match 24.7%; Score 89.5; DB 2; Length 96;
 Best Local Similarity 30.3%; Pred. No. 0.00076;
 Matches 20; Conservative 18; Mismatches 25; Indels 3; Gaps 3;

OY 3 VSPSYRCPCEFFESHVARANKHLKILNT-PNCA-LOIVARLKNNNQVCIDPKLKIQE 60
 DB 27 VANELRCQCLQTVAGIHFKNIQSLKMPGPCHQTEVIATLK-NGREACIDPEAPVYOK 85

OY 61 YLEKAL 66
 DB 86 IVOKML 91

RESULT 13

146871
 Interleukin-8 - rabbit
 N:Alternate names: neutrophil attractant/activation protein-1
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 20-Aug-1999
 C:Accession: I46871; S13052
 R:Yoshimura, T.; Yuhki, N.
 J. Immunol. 146, 3483-3488, 1991

A:title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
 A:Reference number: I46857; M01D:91225489; PMID:2026877
 A:Accession: I46871
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-101 <YOS>
 A:Cross-references: GB:M57439; NID:g165552; PIDN:AAA31422.1; PID:g165553
 R:Beaudien, B.C.; Collins, P.D.; Jose, P.J.; Totty, N.F.; Hsuan, J.; Waterfield, M.D.; W Blochem. J. 271, 797-801, 1990
 A:title: A novel neutrophil chemoattractant generated during an inflammatory reaction in interleukin 8.
 A:Reference number: S13052; M01D:91058518; PMID:2244880

A:Accession: S13052
 A:Molecule type: protein
 A:Residues: 23-33, 'X', '35', 'X', '37-46', 'X', '48-49', 'T', '51-53 <BEA>
 C:Superfamily: beta-thromboglobulin
 C:Keywords: cytokine

Query Match 24.3%; Score 88; DB 2; Length 101;
 Best Local Similarity 28.8%; Pred. No. 0.0012;
 Matches 19; Conservative 21; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSPSYRCPCEFFESHVARANKHLKILNT-PNCA-LOIVARLKNNNQVCIDPKLKI 57
 DB 28 IGTLELRQC--IKTHSPHFHFKIKELRVIESGPHCANSELIYLV-DGRELCIDPEKEM 84

OY 58 IOEYLE 63
 DB 85 VOKVVO 90

RESULT 14

148147
 monocyte chemoattractant protein-1 - guinea pig
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I48147
 R:Yoshimura, T.
 J. Immunol. 150, 5025-5032, 1993

A:title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression
 A:Reference number: I48147; M01D:93267104; PMID:8496603
 A:Accession: I48147
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-120 <RES>
 A:Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
 C:Genetics:
 A:Gene: MCP-1
 C:Superfamily: macrophage inflammatory protein

Query Match 24.3%; Score 88; DB 2; Length 120;
 Best Local Similarity 29.6%; Pred. No. 0.0015;
 Matches 16; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

OY 11 CRFESHVARANKHLKILNTPNCALOIVARLKNNNQVCIDPKLKIOMEYLEK 64
 DB 34 CYTFNKQIPLKRKVGERTTSSRCPEAVIFRLKNEVCADPTOKWODYIAK 87

RESULT 15

JH0200
 macrophage inflammatory protein 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
 C:Accession: JH0200; A32190
 R:Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van J. Exp. Med. 172, 911-919, 1990

A:title: Cloning and characterization of cDNAs for murine macrophage inflammatory pro
 A:Reference number: JH0200; M01D:90354792; PMID:2201751
 A:Accession: JH0200
 A:Molecule type: protein
 A:Residues: 1-100 <TEK>
 A:Cross-references: GB:X53798; NID:g53128; PIDN:CAA37807.1; PID:g53129
 R:Wolpe, S.D.; Sherry, B.; Juers, D.; Davatellis, G.; Yurt, R.W.; Cerami, A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 612-616, 1989
 A:title: Identification and characterization of macrophage inflammatory protein 2.
 A:Reference number: A32190; M01D:89098980; PMID:2643119
 A:Accession: A32190

A:Molecule type: protein
 A:Residues: 28-59 <WOL>
 C:Superfamily: beta-thromboglobulin
 C:Keywords: heparin binding
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-100/Product: macrophage inflammatory protein 2 #status experimental <MAT>

Query Match 23.9%; Score 86.5; DB 2; Length 100;
 Best Local Similarity 30.0%; Pred. No. 0.0019;
 Matches 21; Conservative 19; Mismatches 21; Indels 9; Gaps 4;

OY 3 VSPSYRCPCEFFESHVARANKHLKILNT--PNCA-LOIVARLKNNNQVCIDPKLKI 57
 DB 30 VASELRQCCL--KTLPRVDFKNIQSLSTVPRPGHCAQTEVIATLK-GGKVCIDPEAPL 85

OY 58 IOEYLEKALN 67
 DB 86 VOKIKQILN 95

Search completed: January 23, 2003, 15:37:24
 Job time: 12.6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 ; Search time 6 Seconds

(without alignments)
463.152 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362
Sequence: 1 KGVSPSYRCPCPFESHVAR.....QVCIDPKLKIQIEYLEKALN 67

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT_40:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	344	95.0	93	1 SDF1_FELCA	O62657 felis silve
2	344	95.0	93	1 SDF1_HUMAN	P48061 homo sapien
3	343	94.8	89	1 SDF1_MOUSE	P40324 mus musculu
4	102	28.2	101	1 IL8_CANFA	P41324 canis famill
5	101	27.9	101	1 IL8_CAVPO	P49113 cavia porce
6	99	27.3	101	1 IL8_HUMAN	P09855 felis silve
7	94	26.0	99	1 IL8_HUMAN	P10145 h interleuk
8	93	25.7	101	1 IL8_SHEEP	P36925 ovis aries
9	92.5	25.6	96	1 GRO_MOUSE	P12850 mus musculu
10	92	25.4	103	1 IL8_PIG	P26894 sus scrofa
11	91	25.1	101	1 IL8_MACMU	P51495 macaca mula
12	90.5	25.0	91	1 SY05_MOUSE	P30882 mus musculu
13	90.5	25.0	92	1 SY05_RAT	P50331 rattus norv
14	90	24.9	101	1 IL8_BOVIN	P79255 bos taurus
15	90	24.9	130	1 SZ05_RAT	P97885 rattus norv
16	89.5	24.7	96	1 GRO_RAT	P14095 rattus norv
17	88	24.3	101	1 IL8_RABIT	P19874 oryctolagus
18	88	24.3	120	1 SY02_CAVPO	O08782 cavia porce
19	87.5	24.2	91	1 SY05_CAVPO	P97272 cavia porce
20	87	24.0	100	1 IL8_CERTO	P46653 cercocebus
21	86.5	23.9	100	1 MIR2_MOUSE	P10689 mus musculu
22	85.5	23.6	50	1 SY05_PIG	O29288 sus scrofa
23	85.5	23.6	91	1 SY05_HUMAN	P13501 homo sapien
24	85	23.5	99	1 SY07_HUMAN	P80098 homo sapien
25	82.5	22.8	114	1 SZ06_HUMAN	P80162 homo sapien
26	81.5	22.5	71	1 GRO1_HUMAN	P30782 oryctolagus
27	81.5	22.5	92	1 SY03_RAT	P50229 rattus norv
28	81.5	22.5	100	1 MIR2_RAT	P30348 rattus norv
29	81.5	22.5	112	1 SZ06_BOVIN	P80221 bos taurus
30	81.5	22.4	119	1 SZ07_PIG	P43030 sus scrofa
31	81	22.4	148	1 SY02_MOUSE	P10148 mus musculu
32	81	22.4	148	1 SY02_RAT	P14644 rattus norv
33	80.5	22.2	120	1 SY16_HUMAN	O15467 h small ind

ALIGNMENTS

RESULT 1	ID	SDF1_FELCA	STANDARD:	PRT:	93 AA.
AC	O62657				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DE	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).				
GN	SDF1.				
OS	Felis silvestris catus (Cat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
OX	NCBI_Taxid=9685;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Thymus;				
RX	MEDLINE=98450506; PubMed=9777331;				
RA	Nishimura Y., Miyazawa T., Ikeda Y., Izumiyu Y., Nakamura K.,				
RA	Cai J.S., Sato E., Kohmoto M., Mikami T.;				
RT	"Molecular cloning and sequencing of feline stromal cell-derived				
RT	factor-1 alpha and beta.";				
RL	Eur. J. Immunogenet. 23:303-305(1998).				
CC	-I- FUNCTION: CHEMOKINE-INDUCED T-LYMPHOCYTES, MONOCYTES, BUT				
CC	NOT NEUTROPHILS.				
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);				
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	-I- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE				
CC	C-X-C) (CHEMOKINE CXC).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: AB011966; BAA28602.1; -				
DR	HSSP: P48061; ISDP.				
DR	InterPro: IPR001089; CXC_chemokine_sm11.				
DR	InterPro: IPR001811; Chemokine_IL8.				
DR	Pfam: PF00048; IL8; 1.				
DR	SMART: SM00199; SCY; 1.				
DR	PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.				
KW	Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;				
FT	SIGNAL	1	19	POTENTIAL.	
FT	CHAIN	20	93	STROMAL CELL-DERIVED FACTOR 1.	
FT	DISULFID	30	55	BY SIMILARITY.	
FT	FT	32	71	BY SIMILARITY.	
FT	VARSPLIC	90	93	MISSING (IN ISOFORM ALPHA).	
SO	SEQUENCE	93 AA;	10581 MM;	44FC76371119BE37 CRC64;	
Query Match					
Best Local Similarity 95.0%; Score 344; DB 1; Length 93;					
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					

OY	1	KGVSSTYPCPCPFESHSARAVNHKLKINTPCNALQIYARLKNNNROYCIPDKLKWIDE	60
DB	22	KPVSLSTYPCPCPFESHSARAVNHKLKINTPCNALQIYARLKNNNROYCIPDKLKWIDE	81
OY	61	YLEKALN	67
DB	82	YLEKALN	88
RESULT 2			
ID	SDFL_HUMAN	STANDARD:	PRT; 93 AA.
AC	P48061;		
DT	01-FEB-1996 (Rel. 33, created)		
DT	01-FEB-1996 (Rel. 33, last sequence update)		
DT	15-JUN-2002 (Rel. 41, last annotation update)		
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (hIRH).		
GN	SDFL		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
NP	SEQUENCE FROM N.A.		
RA	Spotila L.D.;		
RL	Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96039262; PubMed=7490086;		
RA	Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,		
RA	Shinozawa T., Honjo T.;		
RT	"Structure and chromosomal localization of the human stromal cell-		
RT	derived factor 1 (SDFL) gene.";		
RL	Genomics 28:495-500(1995).		
RL	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RC	TISSUE=Liver;		
RA	Begun N.A., Barnard G.F.;		
RT	"Nucleotide sequence of hIRH, human interleukin reduced in		
RT	hepatomas.";		
RL	Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.		
RL	[4]		
RP	STRUCTURE BY NMR OF 22-88.		
RX	MEDLINE=96046030; PubMed=9384579;		
RA	Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,		
RA	Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,		
RA	Clark-Lewis I.;		
RT	"Solution structure and basis for functional activity of stromal		
RT	cell-derived factor-1; dissociation of CXCR4 activation from binding		
RT	and inhibition of HIV-1.";		
RL	EMBO J. 16:6996-7007(1997).		
RL	[5]		
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.		
RX	MEDLINE=98284037; PubMed=9618518.		
RA	Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Stani M.A.,		
RA	Lolis E.;		
RT	"Crystal structure of chemically synthesized [N3a] stromal		
RT	cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'		
RT	coreceptor.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).		
CC	-1- FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT		
CC	NOT NEUTROPHILS.		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA AND BETA (SHOWN HERE);		
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.		
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA FAMILY (SMALL CYTOKINE		
CC	C-X-C) (CHEMOKINE CXC).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		

CC entitle requires a license agreement (See http://www.isb-sib.ch/announcement or send an email to license@isb-sib.ch).

DR EMBL; U16752; AAA97434.1; -;
DR EMBL; L36033; AAB39332.1; -;
DR EMBL; L36034; AAB39333.1; -;
DR EMBL; U19495; AAB40516.1; -;
DR PDB; LSDF; 28-JAN-98.
DR PDB; 2SDF; 17-JUN-98.
DR PDB; 1A15; 12-AUG-98.
DR Genew; HGNC:10672; SDF1.
DR InterPro; IPR001089; CXCLCKMLKINE_SMLL.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cyclokin; Chemotaxis; Growth factor; Signal; Alternative splicing;
KW 3d-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 35
FT DISULFID 32 71
FT VARSPIC 90 93 MISSING (IN ISOFORM ALPHA).
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44EBD CRC64;

Query Match 95.0%; Score 344; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 5,3e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSSTGCPGRPFESHAVRANKHLTLNPNCALQIVARLKNNROVCDIPKLKWIQE 60
Db 22 KPVSLSTGPCRFESHSVARANKHLKITLPNCALQIVARLKNNROYCIDPKLKIWE 81

OY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 3
SDFL_MOUSE SDP1_MOUSE STANDARD; PRT; 89 AA.

ID SDP1_MOUSE AC PA0224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPRAL1) (Thymic lymphoma cell stimulating factor) (TUSF).
DE SDF1.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NX NCBI_TaxID=10090;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=94181581; Pubmed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating factor."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN [2]
RP MEDLINE FROM N.A.
RX MEDLINE=93342488; Pubmed=8342023;
RA Tashiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins".
RL Science 261:600-603(1993).
RN [3]
RP MEDLINE FROM N.A.
RX MEDLINE=95073497; Pubmed=7982471;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

RA Weinstein I.B. ;
 RT "Molecular cloning of TPAP1, a gene whose expression is repressed by
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
 RL Exp. Cell Res. 215:284-293(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AKR/J;
 RA Nomura M., Nakata Y., Uzuwa A., Nose M., Akashi M., Suzuki G. ;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DDJJ databases.
 CC -1- FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 CC NOT NEUTROPHILS.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
 CC PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
 CC STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: D21072; BAA04648.1; -
 CC EMBL: L12029; AAA40100.1; -
 CC EMBL: L12030; AAA40101.1; -
 CC EMBL: S74318; AAB32650.1; -
 CC EMBL: D43804; BAA07862.1; -
 CC EMBL: D43805; BAA07863.1; -
 CC PIR: A53497; A53497.
 CC DR HSSP: P48061; 1SDP.
 CC DR MGD: MGI:103556; Sdfl.
 CC DR InterPro: IPR001089; CXC_chemkine_sm11.
 CC DR InterPro: IPR001811; Chemokine_IL8.
 CC DR Pfam: PF00048; IL8; 1.
 CC DR SMART: SM00199; SCY; 1.
 CC DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 CC DR Cytokine: Chemotaxis; Growth factor; Signal; Alternative splicing.
 CC FT SIGNAL 1 19 STROMAL CELL-DERIVED FACTOR 1.
 CC FT CHAIN 20 89 POTENTIAL.
 CC FT DISULFID 30 55 BY SIMILARITY.
 CC FT DISULFID 32 71 BY SIMILARITY.
 CC FT VARSPLIC 89 89 K -> KRLLM (IN ISOFORM BETA).
 CC SQ SEQUENCE 89 AA: 10032 MW: C48BAD69078E55FA CRC64;
 Query Match 94.8%; Score 343; DB 1; Length 89;
 Best Local Similarity 95.5%; Pred. No. 6; 7e-35;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSPYRCPCRFESFHVAVRANKHLINTPCALQIVARLKNRRQVCIDPKLKWIOE 60
 DB 22 KPVSLSYRCPCRFESHIRANVANKHLINTPCALQIVARLKNRRQVCIDPKLKWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88
 RESULT 4
 IL8_CANFA STANDARD: PRT: 101 AA.
 ID IL8_CANFA
 AC P41324;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedes; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010328; PubMed=7916715;
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K. ;
 RT "Cloning of a canine gene homologous to the human
 RL Interleukin-8-encoding gene.";
 RL Gene 131:305-306(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=95127913; PubMed=7827282;
 RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,
 RA Gotsuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshihara K.,
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y. ;
 RT "Molecular cloning and expression of canine interleukin 8 cDNA.";
 RL Cytokine 6:455-461(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mongrel; TISSUE=Jugular vein;
 RX MEDLINE=95114148; PubMed=7814650;
 RA Kukiela G.L., Smith W.C., Larosa G.J., Manning A.M.,
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,
 RA Michael L.H., Rot A., Entman M.L. ;
 RT "Interleukin-8 gene induction in the myocardium after ischemia and
 RL reperfusion in vivo.";
 RL J. Clin. Invest. 95:89-103(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beagle;
 RX MEDLINE=97230298; PubMed=9119462;
 RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J. ;
 RT "Borrelia burgdorferi migrates into joint capsules and causes an up-
 RT regulation of interleukin-8 in synovial membranes of dogs
 RL experimentally infected with ticks.";
 RL Infect. Immun. 65:1273-1285(1997).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: D28772; BAA05961.1; -
 CC EMBL: D14285; BAA03246.1; -
 CC EMBL: U10308; AAC48434.1; -
 CC EMBL: AF048717; AAC05134.1; -
 CC DR HSSP: P10145; 1IKM.
 CC DR InterPro: IPR001089; CXC_chemkine_sm11.
 CC DR InterPro: IPR001811; Chemokine_IL8.
 CC DR Pfam: PF00048; IL8; 1.
 CC DR PRINTS: PR00437; SMALLCYTKCXC.
 CC DR SMART: SM00199; SCY; 1.
 CC DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 CC DR Cytokine: Chemotaxis; Inflammatory response; Signal.
 CC FT SIGNAL 1 22 BY SIMILARITY.
 CC FT CHAIN 23 101 INTERLEUKIN-8.
 CC FT DISULFID 34 61 BY SIMILARITY.
 CC FT DISULFID 36 77 BY SIMILARITY.
 CC SQ SEQUENCE 101 AA: 11280 MW: 3A3A4676DA968376 CRC64;
 Query Match 28.2%; Score 102; DB 1; Length 101;

Best Local Similarity 36.1%; Pred. No. 1.3e-05;
Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;

OY 3 VSPSYRCPCHFFESHVAVAN---VKHLKIINT--PNCALQIYARLKNNNROVCIIDPKLKW 57
DB 28 VSSSLRCQC--IKHTSTPFPKIKELVIDSGPHCENSEIIVKLVN--EVCIDPKRKM 84

OY 58 IOE---YLEKA 65
DB 85 VOKVVOIFLKA 96

RESULT 5
ID IL8_CAVPO STANDARD; PRT; 101 AA.

AC P4913;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein 1) (NAP-1).
GN IL8.

OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
RX MEDLINE=94065176; PubMed=7504015;

RA Yoshimura T., Johnson D.G.;

RT "CDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";

RL J. Immunol. 151:6225-6236(1993)

CC -!- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: L04986; AAA37049.1; -

DR HSSP: P10145; 2118

DR InterPro: IPR001089; CXCL_chemokine_sm11.

DR InterPro: IPR001811; Chemokine_IL8.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTCKXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.

KW Cytokine; Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 101 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.

FT DISULFID 36 77 BY SIMILARITY.

SO SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;

Query Match 27.9%; Score 101; DB 1; Length 101;
Best Local Similarity 35.9%; Pred. No. 1.7e-05;
Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

OY 8 RCRCRPFESHVAVAN---VKHLKIINT--PNCALQIYARLKNNNROVCIIDPKLKW 62
DB 33 RCQC--IKHTSTPFPKIKELVIDSGPHCENSEIIVKLVN--EVCIDPKRKM 89

OY 63 EKAL 66
DB 90 SMFL 93

RESULT 6
ID IL8_FELCA STANDARD; PRT; 101 AA.

AC Q9XSX5;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-8 precursor (IL-8) (CXCL8).

GN IL8.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9685;

RN [1]
RP SEQUENCE FROM N.A.

RA Straubinger A.F., Simpson K.W., Straubinger R.K.;

RT "Feline interleukin-8 mRNA";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: AF158598; AAD40323.1; -

DR HSSP: P10145; 11KM

DR InterPro: IPR001089; CXCL_chemokine_sm11.

DR InterPro: IPR001811; Chemokine_IL8.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTCKXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.

KW Cytokine; Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 101 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.

FT DISULFID 36 77 BY SIMILARITY.

SO SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;

Query Match 27.3%; Score 99; DB 1; Length 101;
Best Local Similarity 33.3%; Pred. No. 2.9e-05;
Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSPSYRCPCHFFESHVAVAN---VKHLKIINT--PNCALQIYARLKNNNROVCIIDPKLKW 57
DB 28 ISSSLRCQC--IKHTSTPFPKIKELVIDSGPHCENSEIIVKLVN--EVCIDPKRKM 84

OY 58 IOEYLE 63
DB 85 VOKVVE 90

RESULT 7
ID IL8_HUMAN STANDARD; PRT; 99 AA.

AC P10145; Q9C077; Q9RG6;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil
 DE chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-
 DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-
 DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emotactin).
 GN IL8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8258376; PubMed=3260265;
 RA Matsushima K., Morishita K., Yoshimura T., Iavii S., Kobayashi Y.,
 RA Lew M., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic
 RT factor (MDNCF) and the induction of MDNCF mRNA by interleukin 1 and
 RT tumor necrosis factor.";
 RL J. Exp. Med. 167:1883-1893(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87224164; PubMed=2953813;
 RA Schmid J., Weissmann C.;
 RT "Induction of mRNA for a serine protease and a
 RT beta-thromboglobulin-like protein in mitogen-stimulated human
 RT leukocytes.";
 RL J. Immunol. 139:250-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89313739; PubMed=2664463;
 RA Kowalski J., Denhardt D.T.;
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating
 RT peptide in differentiating HL60 promyelocytes.";
 RL Mol. Cell. Biol. 9:1946-1957(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89309826; PubMed=2663993;
 RA Mukaida N., Shitoo M., Matsushima K.;
 RT "Genomic structure of the human monocyte-derived neutrophil
 RT chemotactic factor IL-8.";
 RL J. Immunol. 143:1366-1371(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ishikawa J.;
 RT Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Jang J.S., Kim B.E.;
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 23-46.
 RX MEDLINE=89246368; PubMed=2655583;
 RA Golds E.E., Mason P., Nyirkos P.;
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
 RT human synovial cells and fibroblasts.";
 RL Biochem. J. 259:585-588(1989).
 RN [9]
 RP SEQUENCE OF 23-54.
 RX MEDLINE=89279141; PubMed=2659722;
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,
 RA Mizuno S.;
 RT "Purification and partial primary sequence of a chemotactic protein
 RT for polymorphonuclear leukocytes derived from human lung giant cell
 RT carcinoma LU65C cells.";
 RL J. Exp. Med. 169:1895-1901(1989).
 RN [10]
 RP SEQUENCE OF 28-99.
 RX MEDLINE=88162914; PubMed=3279957;
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;
 RT "Structure determination of a human lymphocyte derived neutrophil
 RT activating peptide (LYNAP).";
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).
 RN [11]
 RP SEQUENCE OF 28-59.
 RX MEDLINE=88106502; PubMed=3322281;
 RA Walz A., Feverl P., Aschauer H., Baggiolini M.;
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-
 RT activating factor produced by monocytes.";
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).
 RN [12]
 RP SEQUENCE OF 28-69.
 RX MEDLINE=88097462; PubMed=3480540;
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,
 RA Oppenheim J.J., Leonard E.J.;
 RT "Purification of a human monocyte-derived neutrophil chemotactic
 RT factor that has peptide sequence similarity to other host defense
 RT cytokines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).
 RN [13]
 RP N-TERMINAL FORMS.
 RX MEDLINE=91006326; PubMed=2145175;
 RA van Damme J., Rampart M., Coning R., Decock B., van Osselaer N.,
 RA Willems J., Billiau A.;
 RT "The neutrophil-activating proteins interleukin 8 and beta-
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally
 RT processed forms.";
 RL Eur. J. Immunol. 20:2113-2118(1990).
 RN [14]
 RP N-TERMINAL FORMS.
 RX MEDLINE=89231715; PubMed=2523801;
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;
 RT "Purification of granulocyte chemotactic peptide/interleukin-8
 RT reveals N-terminal sequence heterogeneity similar to that of
 RT beta-thromboglobulin.";
 RL Eur. J. Biochem. 181:337-344(1989).
 RN [15]
 RP SYNTHESIS OF 28-99.
 RX MEDLINE=91175767; PubMed=2007144;
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,
 RA Aebbersold R.;
 RT "Chemical synthesis, purification, and characterization of two
 RT inflammatory proteins, neutrophil activating peptide 1
 RT (interleukin-8) and neutrophil activating peptide.";
 RL Biochemistry 30:3128-3135(1991).
 RN [16]
 RP REVIEW.
 RX MEDLINE=92347562; PubMed=1639201;
 RA Baggiolini M., Clark-Lewis I.;
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";
 RL FEBS Lett. 307:97-101(1992).
 RN [17]
 RP STRUCTURE BY NMR.
 RX MEDLINE=90234679; PubMed=2194886;
 RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;
 RT "Three-dimensional structure of interleukin 8 in solution.";
 RL Biochemistry 29:1689-1696(1990).
 RN [18]
 RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.
 RX MEDLINE=99148123; PubMed=10368283;
 RA Skelton N.J., Quan C., Reilly D., Loman H.;
 RT "Structure of a CXC chemokine-receptor fragment in complex with
 RT interleukin-8.";
 RL Structure 7:157-168(1999).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=90216714; PubMed=2182630;
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,
 RA Wlodawer A., Weber I.T.;
 RT "Crystallization of human interleukin-8. A protein chemotactic for

```

RT  neutrophils and T-lymphocytes."
RL  J. Biol. Chem. 265:6851-6853(1990).
RN  [20]
RX  X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RA  Clore G.M., Gronenborn A.M.;
RT  "Comparison of the solution nuclear magnetic resonance and crystal
RT  structures of interleukin-8. Possible implications for the mechanism
RT  of receptor binding."
RL  J. Mol. Biol. 217:611-620(1991).
RN  [21]
RX  X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RA  Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA  Baldwin M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT  "Crystal structure of interleukin 8: symbiosis of NMR and
RT  crystallography."
RL  Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
RN  [22]
RX  X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RA  Garber N., Lomnan H., Artis D.R., Eigenbrodt C.;
RT  "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT  structure of the LSC/H3C variant at 2.35 A resolution."
RL  Proteins 38:361-367(2000).
CC  -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC  BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC  NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC  RESPONSE TO AN INFLAMMATORY STIMULUS.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXC).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: Y00787; CAA68742.1; -
DR  EMBL: M17017; AAA35611.1; -
DR  EMBL: M26383; AAA36323.1; -
DR  EMBL: M28130; AAA59158.1; -
DR  EMBL: D14283; BAA03245.1; -
DR  EMBL: AF043337; AAK00048.1; -
DR  EMBL: AF385628; AAK60276.1; ALT_SEQ.
DR  PIR: A37034; A37034.
DR  PIR: S03975; S03975.

Query Match      26.0%; Score 94; DB 1; Length 99;
Best Local Similarity 32.3%; Pred. No. 0.00012;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY  8 RCPG-REFRESHAVANVYKILINT-PNCA-IQIVARLKNNNROYCIDPKLWIOEYLEK 64
    11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB  33 RCGIKTKYKRFHPKFIKELRVIESGPHCANTEIIVKL-SGGRRLCDPRENNVQVRVEK 91
    11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY  65 AL 66
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB  92 FL 93

RESULT 8
ID  IL8_SHEEP          STANDARD:      PRT;      101 AA.
AC  P36925;
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-8 precursor (IL-8) (CXCL8).
GN  IL8.

```

```

OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
RN  [1]
RX  SEQUENCE FROM N.A.
RA  MEDLINE=95121931; PubMed=7821808;
RA  Legastelois I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RT  "Sequencing of the ovine interleukin-8-encoding cDNA using the
RT  polymerase chain reaction."
RL  Gene 150:367-369(1994).
RN  [2]
RX  SEQUENCE FROM N.A.
RA  MEDLINE=95137691; PubMed=7835984;
RA  Seow H.F., Yoshimura T., Wood P.R., Golditz I.G.;
RT  "Cloning, sequencing, expression and inflammatory activity in skin of
RT  ovine interleukin-8."
RL  Immunol. Cell Biol. 72:398-405(1994).
CC  -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC  BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC  NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC  RESPONSE TO AN INFLAMMATORY STIMULUS.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXC).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: X78306; CAA55115.1; -
DR  EMBL: S74436; AAB33241.1; -
DR  PIR: S42496; S42496.
DR  HSSP: P10145; 1IKM.
DR  InterPro: IPR001089; CXC_cmkine_sm1.
DR  InterPro: IPR001811; Chemokine_IL8.
DR  Pfam: PF000048; IL8_1; Chemokine_IL8.
DR  PRINTS: PR00437; SMALLCYTKCXC.
DR  SMART: SM00199; SCY_1.
DR  PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW  Cytokine; Chemotaxis; Inflammatory response; Signal.
FT  SIGNAL 1 22 BY SIMILARITY.
FT  CHAIN 23 101 INTERLEUKIN-8.
FT  DISULFID 34 61 BY SIMILARITY.
FT  DISULFID 36 77 BY SIMILARITY.
SQ  SEQUENCE 101 AA; 11292 MW; 40E8418B57C56A5B CRC64;

Query Match      25.7%; Score 93; DB 1; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00016;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

QY  3 VSPSYRCPGFFSFHVARAN---VKHLKILNT-PNCA-IQIVARLKNNNROYCIDPKLW 57
    11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB  28 MSTELKRCQ--IKTHSPFHPKFIKELRVIESGPHCNSBIIVKL-TNGKVEGLDPRKRW 84
    11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY  58 IOEYLEKAL 66
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB  85 VQKVVQAF 93

RESULT 9
ID  GRO_MOUSE          STANDARD:      PRT;      96 AA.
AC  P12850;
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-OCT-1989 (Rel. 12, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Growth regulated protein precursor (CXCL1) (platelet-derived growth
GN  Growth regulated protein precursor (CXCL1) (platelet-derived growth

```

```

Oy      3  VSPSVRCRCRFESHVAVANAKYKHLIL-NPNCNA-LOVARLKKNNRNOVCIDPKXKIOE 60
        ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      27  IANELRCCLOTMAGIHUKNIQSLKVLPSGPHCTOTEVATILK-NGREACDPEAPLVOK 85

Oy      61  YLERAL 66
        ::| |
Db      86  IVOKML 91

RESULT 10
IL8_PIG      STANDARD:      PRT:      103 AA.
AC  P26894:  P22951:
DT  01-AUG-1991 (Rel. 19, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage
DE  chemotactic factor I) (AMCF-I).
GN  IL8.
OS  Sus scrofa (Pig).
OC  Eumaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE-94103307; PubMed-8276681.
RA  Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,
RA  Weiss D.J., Murtough M.P.:
RT  "Regulation of interleukin-8 expression in porcine alveolar
RT  macrophages by bacterial lipopolysaccharide.";
RL  J. Biol. Chem. 269:77-85(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Sanjanwaia M.:
RL  Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.
RC  TISSUE=Lung;
RX  MEDLINE-93041741; PubMed-1420165.
RA  Goodman R.B., Foster D.C., Mathewes S.L., Osborn S.G., Kuiper J.L.,
RA  Forstrom J.W., Martin T.R.:
RT  "Molecular cloning of porcine alveolar macrophage-derived neutrophil
RT  chemotactic factors I and II; Identification of porcine IL-8 and
RT  another interleukin-alpha protein.";
RL  Biochemistry 31:10483-10490(1992).
RN  [4]
RP  REVISION TO 23.
RA  Goodman R.B.:
RL  Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN  [5]
RP  SEQUENCE OF 26-45.
RC  STRAIN=Yorkshire;
RX  MEDLINE-91217086; PubMed-1850745;
RA  Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.:
RT  "Identification of two neutrophil chemotactic peptides produced by
RT  porcine alveolar macrophages.";
RL  J. Biol. Chem. 266:8455-8463(1991).
CC  -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC  BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC  NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC  RESPONSE TO AN INFLAMMATORY STIMULUS.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.
CC  -1- INDUCTION: BY LIPOLYSACCHARIDE (LPS).
CC  -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXC).
CC  -----
CC  THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial

```

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: M66923; AAA1616.1; -
 DR EMBL: X61151; CAA43461.1; -
 DR EMBL: M9367; AAA92576.1; -
 DR PIR: A44253; A44253.
 DR PIR: A39819; A39819.
 DR HSSP: P10145; 1IKM.
 DR InterPro: IPR001089; CXC_chmkine.sm11.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 103 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 FT CONFLICT 33 34 SC -> CR (IN REF. 5).
 FT CONFLICT 87 87 K -> KK (IN REF. 2).
 SQ SEQUENCE 103 AA; 11633 MM; 9PE0E350E1928C64 CRC64;
 Query Match 25.4%; Score 92; DB 1; Length 103;
 Best Local Similarity 31.8%; Pred. No. 0.00021;
 Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;
 QY 3 VSPYRCRPFESHVAVRAN---VKHLKIINT-PNCA-LQIVARLKNNNRQVCDPKLKW 57
 DB 28 VSARLRQC--INTHSPFHPRFKELRVESGPHCENSELIVLV-NGKEVCDPREKW 84
 QY 58 IOEYLE 63
 DB 85 VQKVVO 90
 RESULT 11
 IL8_MACMU
 ID IL8_MACMU STANDARD; PRT; 101 AA.
 AC P51495;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Macaca mulatta (Rhesus macaque), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544; 9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 RT nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; TISSUE=Blood;
 RX MEDLINE=95355132; PubMed=7628861;
 RA Miniere J.C., Baganoff M.P., Deppele C.L., Keller B.T.,
 RA Rapp S.R., Wlodek D.L., Fretland D.J., Bolanowski M.A.;
 RT "Identification and characterization of rhesus macaque
 RT Interleukin-8.";
 RL Inflammation 19:313-331(1995).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: U19849; AAA86711.1; -
 DR EMBL: U19851; AAA86713.1; -
 DR EMBL: S78555; AAA80141.2; -
 DR HSSP: P10145; 2IL8.
 DR InterPro: IPR001089; CXC_chmkine.sm11.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 101 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11320 MM; 42BCF9C97C84B5F9 CRC64;
 Query Match 25.1%; Score 91; DB 1; Length 101;
 Best Local Similarity 31.7%; Pred. No. 0.00028;
 Matches 19; Conservative 18; Mismatches 19; Indels 4; Gaps 4;
 QY 8 RCPG-RFESHVAVRANVKHLKIINT-PNCA-LQIVARLKNNNRQVCDPKLWIOEYLEK 64
 DB 33 RCRCIKTYSPFHPRFKELRVESGPHCANTETIVLV-SDGRCLCDPREWQRYVER 91
 RESULT 12
 SY05_MOUSE
 ID SY05_MOUSE STANDARD; PRT; 91 AA.
 AC P30882;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A5 precursor (CCU5) (T-cell specific RANTES
 DE protein) (SIS-delta) (Murantes).
 GN SCYAS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92277990; PubMed=1375672;
 RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
 RA Krensky A.M., Neilson E.G.;
 RT "Isolation and characterization of cDNA from renal tubular epithelium
 RT encoding murine Rantes.";
 RL Kidney Int. 41:220-225(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92289805; PubMed=1376260;
 RA Schall T.J., Simpson N.J., Mak J.Y.;
 RT "Molecular cloning and expression of the murine RANTES cytokine:
 RT structural and functional conservation between mouse and man.";
 RL Eur. J. Immunol. 22:1477-1481(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss;
 RX MEDLINE=94132613; PubMed=7507961;
 RA Danoff T.M., Talley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
 RT "Cloning, genomic organization, and chromosomal localization of the

```

RT SCy5 gene encoding the murine chemokine RANTES."
RL J Immunol. 152:1182-1189(1994).
(4)
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/C;
RX MEDLINE=94217689; PubMed=7513046;
RA Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,
Paznekas W.A.;
RT "Definition of a lipopolysaccharide-responsive element in the 5'-
RL flanking regions of Murantes and crg-2."
RL Mol. Cell. Biol. 14:2914-2925(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/C; BIO.S/J, MOD/LTJ, and SJL/J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
DR EMBL: M77747; AAA40029.1; -
DR EMBL: S37648; AAB22330.1; -
DR EMBL: U02298; AAA18302.1; -
DR EMBL: X70675; CAA50011.1; -
DR EMBL: AF065944; AAC17511.1; -
DR EMBL: AF065945; AAC17512.1; -
DR EMBL: AF065946; AAC17513.1; -
DR EMBL: AF065947; AAC17514.1; -
DR HSSP: P13501; IRTN.
DR MGD: MGI:98262; SCy5.
DR InterPro: IPR000827; CC:chemokine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
FT CONFLICT 19 19 T -> A (IN REF. 2).
FT CONFLICT 41 41 A -> E (IN REF. 1).
SQ SEQUENCE 91 AA; 10071 MW; 5DFD66F4684FE1C8 CRC64;

Query Match 25.0%; Score 90.5; DB 1; Length 91;
Best Local Similarity 38.2%; Pred. No. 0.00028;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

OY 10 PCRFESHVA--RANKHLKIINTPNCALQIYARLKNNNROYCIDPKLKWIOEYL 62
DB 32 PCCFAVLISLAPRAHKEY-FYTSSKSCNMLAVFVTRNRROYCANPEKRWQVEYI 85

RESULT 13
SY05_RAT STANDARD; PRT; 92 AA.
AC P50231.
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES

```

```

DE protein) (SIS-delta).
GN SCY5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RA Jones M.L., Shanley T.P., Ward P.A.;
RL Submitted (Feb-1994) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
DR EMBL: U06436; AAA96499.1; -
DR HSSP: P13501; IRTN.
DR InterPro: IPR000827; CC:chemokine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A5.
FT DISULFID 34 58 BY SIMILARITY.
FT DISULFID 35 74 BY SIMILARITY.
SQ SEQUENCE 92 AA; 10170 MW; B4FBC2B4208A9C6 CRC64;

Query Match 25.0%; Score 90.5; DB 1; Length 92;
Best Local Similarity 38.2%; Pred. No. 0.00029;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

OY 10 PCRFESHVA--RANKHLKIINTPNCALQIYARLKNNNROYCIDPKLKWIOEYL 62
DB 33 PCCFAVLISLAPRAHKEY-FYTSSKSCNMLAVFVTRNRROYCANPEKRWQVEYI 86

RESULT 14
ID IL8_BOVIN STANDARD; PRT; 101 AA.
AC P79255;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96304552; PubMed=8737490;
RA Morsey M.A., Popowycz Y., Kowalski J., Gerlach G., Godson D.,
RA Campos M., Babiuk L.A.;
RT "Molecular cloning and expression of bovine Interleukin-8."
RL Microb. Pathog. 20:203-212(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Galligan C.L., Yoshimura T., Coomber B.L.;

```

RT "Cloning and sequencing of bovine interleukin 8 cDNA isolated from
RT lipopolysaccharide stimulated monocytes in vitro."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; S82598; AAB37483.1; -.
DR EMBL; AF232704; AAF37575.1; -.
DR HSSP; P10145; 1IKM.
DR InterPro: IPR001089; CXK_cmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCXK.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22
FT CHAIN 23 101
FT DISULFID 34 61
FT DISULFID 36 77
SQ SEQUENCE 101 AA: 11291 MW: 061A530507906736 CRC64:

Query Match 24.9%; Score 90; DB 1; Length 101;
Best Local Similarity 30.3%; Pred. No. 0.00036;
Matches 20; Conservative 20; Mismatches 18; Indels 8; Gaps 5;

QY 3 VSPSYRCPCRFESHVAVRAN---VKHLKIINT-PNCA-LQIVARLKNNNROYCIDPKLKW 57
DB 28 MSTELKQCQ--IKTSTPHPKFKELRVIESGPHCENSEIIVKLTNGN-EVCLNPKRW 84
QY 58 IOEYLE 63
DB 85 VQKVQ 90

RESULT 15
S205_RAT ID S205_RAT STANDARD; PRT; 130 AA.
AC P97885;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).
GN SCYB5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Kelnher G.S., Maciejewski-Lenoir D., Lee E.D., Maki R.A.;
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: MAY PARTICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS
CC BY INJURED OR INFECTED TISSUE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U90448; AAB61460.1; -.
DR HSSP; P10889; 1M12.
DR InterPro: IPR001089; CXK_cmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCXK.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Signal.
FT SIGNAL 1 37
FT CHAIN 38 130
FT DISULFID 50 76
FT DISULFID 52 93
SQ SEQUENCE 130 AA: 14263 MW: C00F6B3605524F4E CRC64;

Query Match 24.9%; Score 90; DB 1; Length 130;
Best Local Similarity 27.3%; Pred. No. 0.00047;
Matches 18; Conservative 19; Mismatches 27; Indels 2; Gaps 2;

QY 3 VSPSYRCPCRFESHVAVRANVKHLKIINT-PNC-ALQIVARLKNNNROYCIDPKLWIOE 60
DB 44 VATELRCVCLTLAPRLNPKMIANLEVIYIPAGPHCKVEYIAKLKNQNDVCLDPQAPLKK 103
QY 61 YLEKAL 66
DB 104 VIOKIL 109

Search completed: January 23, 2003, 15:34:18
Job time : 6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 : Search time 22.6 Seconds
(without alignments)
610.848 Million cell updates/sec

Title: US-09-852-424-2
Perfect score: 362
Sequence: 1 KGVSPSYRCPCRFESHVAR.....QVCIDPKLKIQETLEKALN 67

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_fodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriopl:*
17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.0	92	4 Q9H554	Q9H554 homo sapien
2	336	92.8	89	11 Q9QZD1	Q9QZD1 ratius norv
3	278	76.8	94	13 Q8U0U9	Q8U0U9 xenopus lae
4	93.5	25.8	91	11 Q91ZL1	Q91ZL1 sigmodon hi
5	85	23.5	98	13 Q8QCV8	Q8QCV8 paraliichthy
6	85	22.5	109	13 Q90Y59	Q90Y59 paraliichthy
7	81	22.4	104	13 Q73912	Q73912 gallus galli
8	81	22.4	134	12 Q9YV93	Q9YV93 gallus galli
9	81	22.4	142	12 Q91B77	Q91B77 turkey herp
10	81	22.4	203	12 Q67634	Q67634 mus musculu
11	80	22.1	148	11 Q9QXD7	Q9QXD7 mus musculu
12	79.5	22.0	101	13 Q83442	Q83442 lampetra fi
13	79.5	22.0	108	6 Q28724	Q28724 oryctolagus
14	79	21.8	97	13 Q98TQ2	Q98TQ2 oncorhynch
15	78.5	21.7	100	11 Q912K9	Q912K9 sigmodon hi
16	77.5	21.4	97	13 Q8QFP5	Q8QFP5 cyprinus ca

17	77	21.3	79	4 Q95689	Q95689 homo sapien
18	76.5	21.1	101	11 Q91264	Q91264 sigmodon hi
19	76	21.0	106	11 Q92292	Q92292 cricetus
20	74.5	20.6	363	13 Q90ZT0	Q90ZT0 brachydanio
21	74.5	20.6	1096	13 Q90ZT1	Q90ZT1 brachydanio
22	73.5	20.3	97	11 Q92318	Q92318 cavia porce
23	73.5	20.3	126	11 Q99J60	Q99J60 mus musculu
24	72.5	20.0	883	13 Q91493	Q91493 torpedo cal
25	72	19.9	89	13 Q918R0	Q918R0 gallus galli
26	72	19.9	101	13 Q8UW91	Q8UW91 tritakis scy
27	71	19.6	96	13 Q90825	Q90825 gallus galli
28	70.5	19.5	91	13 Q8Q656	Q8Q656 gallus galli
29	70.5	19.5	601	13 Q73928	Q73928 scyllorhinu
30	70	19.3	91	13 Q8Q657	Q8Q657 gallus galli
31	70	19.3	95	12 Q88158	Q88158 xiposotis sa
32	69.5	19.2	97	6 Q9TTS6	Q9TTS6 bos taurus
33	69	19.1	80	4 Q14745	Q14745 homo sapien
34	69	19.1	92	6 Q8SQ40	Q8SQ40 felis silve
35	69	19.1	93	4 Q96168	Q96168 homo sapien
36	69	19.1	395	11 Q91V44	Q91V44 mus musculu
37	68.5	18.9	92	11 Q91Z65	Q91Z65 sigmodon hi
38	68.5	18.9	101	11 Q9EP62	Q9EP62 ratius norv
39	68	18.8	102	6 Q95M27	Q95M27 ovis aries
40	67.5	18.6	116	11 Q91ZB2	Q91ZB2 mus musculu
41	67	18.5	507	10 Q23757	Q23757 beta vulgar
42	66	18.2	240	2 Q9Z910	Q9Z910 magnetospor
43	65.5	18.1	100	13 Q8Q637	Q8Q637 oncorhynch
44	65.5	18.1	150	11 Q9QW66	Q9QW66 mus sp. dys
45	65.5	18.1	258	11 Q9D6J7	Q9D6J7 mus musculu

ALIGNMENTS

RESULT 1
ID Q9H554 PRELIMINARY: PRT: 92 AA.
AC Q9H554:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)
DE (Fragment).
GN SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137026; CAC10202.1; -
DR HSSP; P48061; ISDF.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
FT NON-TER
SQ SEQUENCE 92 AA: 10510 MN; AEF0C402B44EBD20 CRC64;

Query Match Best Local Similarity 95.0%; Score 344; DB 4; Length 92;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIE 60
DB 22 KGVSPSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

ID	Q9QZD1	PRELIMINARY:	PRT:	89 AA.
AC	Q9QZD1			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	Stromal cell-derived factor-1 alpha.			
GN	SDF-1.			
OS	Rattus norvegicus (rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
OX	NCBI_TaxID=10116;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY;			
RA	Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;			
RT	"cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1			
RT	alpha).";			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RA	Pillarsetti K., Gupta S.K.;			
RT	"Identification and molecular cloning of a novel rat ortholog of the			
RT	alpha chemokine, stromal cell derived factor-1 (SDF-1).";			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF189724; AAF01066.1; -.			
DR	EMBL: AF209976; AAG43506.1; -.			
DR	HSSP: P48061; 1SDF.			
DR	InterPro: IPR001811; Chemokine_IL8.			
DR	Pfam: PF00048; IL8; 1.			
DR	SMART: SM00199; SCY; 1.			
SO	SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;			
	Query Match	92.8%;	Score 336;	DB 11; Length 89;
	Best local similarity	94.0%;	Pred. No. 1.8e-34;	
	Matches 63; Conservative	2;	Mismatches 2;	Indels 0; Gaps 0
QY	1 KGVSPSYRCPCHFFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60			
DB	22 KPVSLSYRCPCHFFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 81			
QY	61 YLEKALN 67			
DB	82 YLDKALN 88			
RESULT 3				
Q8U0J9	PRELIMINARY:	PRT:	94 AA.	
AC	Q8U0J9			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Stromal-derived factor 1 precursor.			
GN	SDF-1.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=83355;			
OX	NCBI_TaxID=83355;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPLEEN;			
RA	Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;			
RT	"Xenopus laevis stromal-derived factor 1: conservation of structure			
RT	and function during vertebrate development.";			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AJ278857; CAC62196.1; -.			
DR	InterPro: IPR001811; Chemokine_IL8.			
DR	Pfam: PF00048; IL8; 1.			
DR	SMART: SM00199; SCY; 1.			
DR	Signal.			

FT	CHAIN	1	21	POTENTIAL.
FT	CHAIN	22	94	STROMAL-DERIVED FACTOR 1.
SO	SEQUENCE	94 AA.	10701 MW;	8C8325D152F326E7 CRC64;
Query Match				
Best Local Similarity		76.8%;	Score 278;	DB 13; Length 94;
Matches 49;		Conservative 11;	Mismatches 7;	Indels 0; Gaps 0;
OY	1	KGVSSTYGCPCPFESHSARANKLILTPNCALQIYARKNNRQYCIDPKLKIOWE	60	
DB	22	KPVSLVYRCPCPYFESVNPVSKNIKLITLSTNSCLQIYARKLHNGKQICLDPKTKIOWE	81	
OY	61	YLEKALN	67	
DB	82	YLEKALN	88	
RESULT 4				
O91ZL1	PRELIMINARY;	PRT;	91 AA.	
ID	O91ZL1			
AC	O91ZL1			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)			
DE	RANTES chemokine.			
OS	Sigmodon hispidus (Hispid cotton rat).			
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;			
CC	Sigmodon.			
OX	NCBI_TaxID=42415;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Blanco J.C., Plateney L.M., Prince G.A.;			
RT	"Submitted hispidus cytokines, chemokines and interferons."			
RL	Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF421391; AAL16932.1; -			
DR	InterPro; IPR000827; CC_chemkine.sm1.			
DR	InterPro; IPR001811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN_1.			
SO	SEQUENCE 91 AA; 10082 MW; D0D6EABABE4242FF CRC64;			
Query Match				
Best Local Similarity		25.8%;	Score 93.5;	DB 11; Length 91;
Matches 21;		Conservative 9;	Mismatches 22;	Indels 3; Gaps 2;
OY	10	PCRF-FESHARANKVHLKILTPNCALQIYARKNNRQYCIDPKLKIOWEYL	62	
DB	32	PCCFYVLSAVLPERAHKEY-FYTSSKCSNFAVVFYTRNRQVCANPKKRWGEYL	85	
RESULT 5				
O80GV8	PRELIMINARY;	PRT;	98 AA.	
ID	O80GV8			
AC	O80GV8			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	CXC chemokine.			
GN	CXC CHEMOKINE.			
OS	Paralichthys olivaceus (Flounder).			
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
CC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;			
CC	Pleuronectoidae; Paralichthyidae; Paralichthys.			
OX	NCBI_TaxID=8255;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Aoki T., Hirono I., Lee J., Iwahori A.;			
RT	"Molecular cloning and expression of IL-1b and two types of chemokines			
RL	in Japanese flounder, Paralichthys olivaceus."			
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.			
EMBL	AB070837; BAB6884.1; -			

SO	SEQUENCE	98 AA:	10846 MW:	4959CA4839A5D8C92 CRC64:
QY	1 KGVSSTVPCPCFFFSHARAVNKKLILNPN--C-ALQIYARLKNNRQVCIDPKLKW	57		
DB	27 RSLGVSLLHCRCTETESRPIGRYIKSVETI-SPNSHCDKTEIATLKDGVELCLDPEAPW	85		
QY	58 IOEYLEKALN 67			
DB	86 VKRIVNKILIS 95			
RESULT 6				
ID	090Y59	PRELIMINARY:	PRT:	109 AA.
AC	090Y59:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Interleukine-8.			
GN	IL-8.			
OS	Paralichthys olivaceus (Flounder).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorphi; Acanthopterygii; Percomorpha; Pleuronectiformes;			
OC	Pleuronectoidae; Paralichthyidae; Paralichthys.			
OX	NCBI_TaxID=8255;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=21435923; PubMed=11551708;			
RT	Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;			
RT	"Cloning and sequence analysis of the interleukin-8 gene from flounder			
RL	(Paralichthys olivaceus).";			
DR	Gene 274:237-243(2001).";			
DR	EMBL; AF216646; AAL05442.1; "			
DR	InterPro; IPR001811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
SO	SEQUENCE 109 AA: 12117 MW: C7CE18986C50A6ED CRC64:			
QY	1 KGVSSTVPCPCFFFSHARAVNKKLILNPN--C-ALQIYARLKNNRQVCIDPKLKW	57		
DB	26 RSLGVSLLHCRCTETESRPIGRYIKSVETI-SPNSHCDKTEIATLKDGVELCLDPEAPW	84		
QY	58 IOEYLEKALN 67			
DB	85 VKRIVNKILIS 94			
RESULT 7				
ID	073912	PRELIMINARY:	PRT:	104 AA.
AC	073912:			
DT	01-AUG-1998 (TREMBLrel. 07, Created)			
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	K60 protein precursor (CXC chemokine K60).			
GN	Gallus gallus (Chicken).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	TISSUE=MACROPHAGE LIKE;			
RA	Sick C.;			

```

RN Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RP
RX MEDLINE=20170941; Pubmed=10704244;
RA Slick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXC and CC chemokines.";
RL Cytokine 12:181-186(2000).
RN
RP
RA HUGHES S.M., BUNSTEAD N.;
RT "Mapping of a second ELR CXC chemokine to chicken chromosome four.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y14971; CAA75212.1; -.
DR EMBL; AF277660; AAF66485.1; -.
DR HSSP; P02775; 1P7V.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_Chmkine_smll.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTCCXC.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SO SEQUENCE
Query Match 22.4%; Score 81; DB 13; Length 104;
Best Local Similarity 29.2%; Pred. No. 0.016;
Matches 19; Conservative 18; Mismatches 20; Indels 8; Gaps 4;
OY 8 RCPCHESHVARANKHLKILNT---PNCALQIVARKNNNOVCIDPKLKIQEYL 62
Db 33 RCQC--IETHSKFHPKFIQNVNLTSPSGPHCKNVEIATLK-DGREVCIDPTAPWVKLI 89
OY 63 EKALN 67
Db 90 KAILD 94
RESULT 8
O9YVA9 PRELIMINARY; PRT; 134 AA.
AC O9YVA9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE VIL8 (CXC chemokine VIL8).
GN MDV003 OR MDV078.
OS Gallid herpesvirus 1,
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Marek's disease herpesvirus (strain Md5) (MDV). Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
NCBI TaxID=103386, 103386, 103389;
RN
RP
RA "SEQUENCE FROM N.A.
RA SPECIES=galid herpesvirus 1; STRAIN=RB18;
RA Rasschaert D., Fagnat L.;
RT "Characterisation of the BamH I fragment of the Marek's disease virus
RT RB18 strain (serotype 1).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN
RP
RA "SEQUENCE FROM N.A.
RA SPECIES=Marek's disease herpesvirus (strain GA) (MDHV);
RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.;
RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN
RP
RA "SEQUENCE FROM N.A.
RA SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);
RA MEDLINE=20392152; Pubmed=10533706;
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
```

RL J. Virol. 74:7980-7988(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SUBJECTS-Marek's disease herpesvirus (strain M65) (MDV);
 RA Tullman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF314199; AAL58097.1; -
 DR EMBL: AF065430; AAC77449.1; -
 DR EMBL: AF243438; AAC14290.1; -
 DR EMBL: AF243438; AAC14256.1; -
 DR HSP: P10889; IM12.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKXC.
 DR SMART: SM00199; SCY; 1.
 SQ SEQUENCE 134 AA; 1482 MW; C859CDB868D25190 CRC64;
 Query Match 22.4%; Score 81; DB 12; Length 134;
 Best Local Similarity 25.7%; Pred. No. 0.021;
 Matches 19; Conservative 13; Mismatches 10; Indels 32; Gaps 4;
 QY 8 RCPREFESHVARANVHKLILNTP-----NC-ALQIVARLKNRRQVC 50
 DB 33 RCKC-----VKVTNRPGLPIAVDVIPGICHRTETITALK-KNRKVC 77
 QY 51 IDPKLWIOEYLEK 64
 DB 78 VDPEAPWVOQFIKK 91
 RESULT 9
 Q9IBJ7 PRELIMINARY; PRT; 142 AA.
 AC 09IBJ7;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE VIL-8.
 GN R-LORE2.
 OS Turkey herpesvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OC NCBI_TaxID=10386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GA;
 RX MEDLINE-92237304; PubMed=1315048;
 RA Jones D., Lee L., Liu J.L., Kung H.J., Tilletson J.K.;
 RT "Marek disease virus encodes a basic-leucine zipper gene resembling
 RT the fos/ Jun oncogenes that is highly expressed in lymphoblastoid
 RT tumors";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GA;
 RA Lee L.F., Wu P., Sul D., Ren D., Kung H.J.;
 RT "The Complete U. Sequence of Serotype I Marek's Disease Virus";
 RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
 DR EMBL: AF147806; AAF67205.1; -
 DR EMBL: AF147806; AAF67205.1; -
 DR HSP: P10889; IM12.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKXC.
 DR SMART: SM00199; SCY; 1.
 SQ SEQUENCE 142 AA; 15770 MW; 35A8CEB8B29FDD209 CRC64;
 Query Match 22.4%; Score 81; DB 12; Length 142;
 Best Local Similarity 25.7%; Pred. No. 0.022;

Matches 19; Conservative 13; Mismatches 10; Indels 32; Gaps 4;
 QY 8 RCPREFESHVARANVHKLILNTP-----NC-ALQIVARLKNRRQVC 50
 DB 33 RCKC-----VKVTNRPGLPIAVDVIPGICHRTETITALK-KNRKVC 77
 QY 51 IDPKLWIOEYLEK 64
 DB 78 VDPEAPWVOQFIKK 91
 RESULT 10
 Q67634 PRELIMINARY; PRT; 203 AA.
 AC 067634;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Eco Q protein (Fragment).
 OS Marek's disease herpesvirus (strain GA) (MDV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OC NCBI_TaxID=10386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GA;
 RX MEDLINE-96074534; PubMed=7491783;
 RA Peng Q., Zeng M., Bhuyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
 RA Shirazi Y.;
 RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
 RT mapping to the BamHI-12, BamHI-Q2, and BamHI-L fragments of the MDV
 RT genome from lymphoblastoid cells transformed and persistently infected
 RT with MDV";
 RL Virology 213:590-599(1995).
 DR EMBL: U34966; AAC54629.1; -
 DR HSP: P10889; IM12.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12.
 DR InterPro: IPR004827; TF_bZIP.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKXC.
 DR SMART: SM00338; BRIZ; 1.
 DR SMART: SM00199; SCY; 1.
 FT NON_TER 1
 SQ SEQUENCE 203 AA; 23132 MW; DE42F2A1C1A71C88 CRC64;
 Query Match 22.4%; Score 81; DB 12; Length 203;
 Best Local Similarity 25.7%; Pred. No. 0.032;
 Matches 19; Conservative 13; Mismatches 10; Indels 32; Gaps 4;
 QY 8 RCPREFESHVARANVHKLILNTP-----NC-ALQIVARLKNRRQVC 50
 DB 102 RCKC-----VKVTNRPGLPIAVDVIPGICHRTETITALK-KNRKVC 146
 QY 51 IDPKLWIOEYLEK 64
 DB 147 VDPEAPWVOQFIKK 160
 RESULT 11
 Q9QYD7 PRELIMINARY; PRT; 148 AA.
 AC 09QYD7;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Small inducible cytokine A2.
 GN SCY42.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-SJL/J: TISSUE=SPLEEN;
RX MEDLINE=96370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Sclay1 (TCA-3), Sclay2
RT (monocyte chemoattractant protein (MCP)-1), and Sclay12 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis."
RL J. Immunol. 163:2262-2266(1999).
DR EMBL: AF065929; AAF15379.1; -.
DR HSSP: P13500; 1DOK.
DR MGS: MGI:98259; Sclay2.
DR InterPro: IPR000827; CC_Chemokine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489EB CRC64;

Query Match
Best Local Similarity 22.1%; Score 80; DB 11; Length 148;
Matches 15; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

Oy 3 VSPSYRCPGFESHVARANVHKILMTNPNCALQIVARLKNNNROYCDIPKWKIOEYL 62
   1: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 28 VNAPLTCCSFYSKMLPMSRLBEGYKRTTSRCPEAVVETKLRKVCADPKKRWOTYI 87
   1: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 63 E 63
Db 88 K 88

RESULT 12
O93442
ID 093442; PRELIMINARY; PRT; 101 AA.
AC 093442;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE LFCA-1 protein precursor.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_Taxid=7748;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEUCOCYTES;
RA Najakshin A.M., Mechetina L.V., Alabeyev B.Y., Tarantin A.V.;
RT "Identification of the interleukin 8 homologue in lamprey (Lampetra
RT fluviatilis): early evolutionary divergence of chemokines."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ231072; CAA1314.1; -.
DR HSSP: P02775; 1TVX.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL12; 1.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1.
DR SIGNAL.
KW Signal.
FT CHAIN 23 101 LFCA-1 PROTEIN.
SQ SEQUENCE 101 AA; 11095 MW; 80CFEB1EA7336D2 CRC64;

Query Match
Best Local Similarity 22.0%; Score 79.5; DB 13; Length 101;
Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;

Oy 8 RCRCRFESHVARANV-KHLK----ILNTPNCA-LQIVARLKNNNROYCDIPKWKIOEYL 60
   1: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30 RCOC----VAVISKFTHPKHFTMEVYIPSSNCKNVEIIVTMKSTNNQICLNDAFVVRK 85
   1: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 YLEKALN 67

```

```

Db 86 VISHILD 92

RESULT 13
O28724
ID 028724; PRELIMINARY; PRT; 108 AA.
AC 028724;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE GRO (Permeability factor 2).
GN RPF2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RA Yoshimura T., Modi W.S.;
RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXCL
RT chemokine subfamily in mammals."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 43-108 FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RX MEDLINE=95129889; PubMed=7828903;
RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA Martin T.R.;
RT "Cloning of two rabbit GRO homologues and their expression in alveolar
RT macrophages."
RL Gene 151:337-338(1994).
DR EMBL: U95808; AAB93924.1; -.
DR EMBL: L28933; AAB6975.1; -.
DR HSSP: P19875; 1ONK.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL12; 1.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 108 AA; 11261 MW; 9C2780A1FC7A5BAD CRC64;

Query Match
Best Local Similarity 22.0%; Score 79.5; DB 6; Length 108;
Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

Oy 8 RCRCRFESHVARANVHKILMT-PNCA-LQIVARLKNNNROYCDIPKWKIOEYLEKA 65
   1: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 RCOCLOTGVCIHLSKISLSPGPHCAQTEVIATLK-SGQECINPAAPVKKFLQKR 101
   1: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 66 LN 67
Db 102 LS 103

RESULT 14
O98702
ID 098702; PRELIMINARY; PRT; 97 AA.
AC 098702;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative interleukin 8 (Putative cxc chemokine precursor).
GN IL-8.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei.
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_Taxid=8022;
RN [1]
RP SEQUENCE FROM N.A.

```


PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 XX WPI: 2002-106073/14.
 DR
 PT Promoting the rate of haematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 XX
 PS Claim 9; Page 54; 68pp; English.
 XX
 CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 CC
 XX
 SQ Sequence 67 AA;
 QY
 Query Match 100.0%; Score 362; DB 23; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2.7e-40;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 KGVSLPFCPCRFESHVARANYKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
 QY 61 YLEKALN 67
 DB 61 YLEKALN 67
 DE CXCR4 peptide antagonist SEQ ID NO 1.
 XX
 DE CXCR4 peptide antagonist SEQ ID NO 1.
 XX
 KW CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.
 XX
 OS Synthetic.
 XX
 PN WO200185196-A2.
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001; 2001WO-CA00659.
 XX
 PR 09-MAY-2000; 2000CA-2305787.
 PR 19-MAY-2000; 2000US-205467P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 XX WPI: 2002-106073/14.
 XX

PT Promoting the rate of haematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 XX
 PS Claim 9; Page 54; 68pp; English.
 XX
 CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 CC
 XX
 SQ Sequence 67 AA;
 QY
 Query Match 97.8%; Score 354; DB 23; Length 67;
 Best Local Similarity 98.5%; Pred. No. 3.1e-39;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 KGVSLPFCPCRFESHVARANYKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
 QY 61 YLEKALN 67
 DB 61 YLEKALN 67
 DE CXCR4 peptide antagonist SEQ ID NO 2.
 XX
 DE CXCR4 peptide antagonist SEQ ID NO 2.
 XX
 KW CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.
 XX
 OS Synthetic.
 XX
 PN WO200185196-A2.
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001; 2001WO-CA00659.
 XX
 PR 09-MAY-2000; 2000CA-2305787.
 PR 19-MAY-2000; 2000US-205467P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 XX WPI: 2002-106073/14.
 XX

PT	Promoting the rate of haematopoietic cell multiplication for treating a
PT	cancer involves administering chemokine receptor antagonist to the
PT	cells -
PS	
PS	ClaIm 9; page 54; 68pp; English.
XX	
CC	The invention relates to a method of promoting the rate of haematopoietic
CC	cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC	antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC	has cytostatic and immunosuppressive activity and is useful for treating
CC	cancer or autoimmune disease in a patient; to promote the rate of
CC	haematopoietic cell multiplication; to formulate a medicament for
CC	increasing the circulation of the haematopoietic cells in a patient; for
CC	mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC	locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC	CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC	self-renewal, expansion and proliferation of peripheralisation in vivo.
XX	
XX	Sequence 67 AA:
SO	
Query Match	95.98; Score 347; DB 23; Length 67;
Best Local Similarity	97.0%; Pred. No. 2.6e-38;
Matches 65; Conservative	0; Mismatches 2; Indels 0; Caps
QY	1 KGVSLPRCPREFESHVARANVNHKILTPNCALDITVARLKNKNNOVCIDPKLKIOE 60
DB	1 KGVSPTRCPREFESHVARANVNHKILTPNCALDITVARLKNKNNOVCIDPKLKIOE 60
QY	61 YLEKALN 67
DB	61 YLEKALN 67
RESULT 4	
AAM48660	standard; peptide; 67 AA.
XX	
XX	AAM48660:
XX	
XX	20-MAY-2002 (first entry)
DE	CXCR4 peptide antagonist SEQ ID NO 5.
KW	CHCX4: haematopoietic cell; chemokine receptor-4; cytostatic;
KW	immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
XX	cell multiplication.
OS	Synthetic.
XX	
XX	Key Location/Qualifiers
FT	Modified-site 8
FT	/note="Optionally the proline analogue 6-amino-7-oxo-2-
FT	3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
FT	acid residue"
XX	
XX	WO200185196-A2.
XX	
XX	15-NOV-2001.
XX	
XX	09-MAY-2001; 2001WO-CA00659.
XX	
XX	09-MAY-2000; 2000CA-2305787.
XX	19-MAY-2000; 2000US-205467P.
XX	
XX	(UYBR-) UNIV BRITISH COLUMBIA.
XX	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX	
XX	Tudan CR, Mertzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
XX	Clark-Lewis I, Salaria H;
XX	
XX	WPI; 2002-106073/14.
XX	
XX	Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the
PT cells - English.

XX Claim 9; Page 54; 68pp; English.
PS

CC The invention relates to a method of promoting the rate of haematopoietic
CC cell multiplication comprising administering chemokine receptor-4 (CXCR
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC has cytostatic and immunosuppressive activity and is useful for treatin
CC cancer or autoimmune disease in a patient; to promote the rate of
CC haematopoietic cell multiplication; to formulate a medicament for
CC increasing the circulation of the haematopoietic cells in a patient;
CC mobilising haematopoietic cells from a narrow locus to a peripheral blo
CC locus; In the treatment of haematopoietic cells in vitro and in vivo. T
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC self-renewal, expansion and proliferation of peripheralisation in vivo.
CC XX

SQ Sequence 67 AA:

Query Match 95.9%; Score 347; DB 23; Length 67;
Best Local Similarity 97.0%; Pred. No. 2,6e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps

OY 1 KGVSLPYRCRPFESHVARANVKHLKLTLPNCALQIVARLKNRRVCIDPKLKWIOE 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 KGVSLSPYPCRFESHVARANVKHLKLTLPNCALOIVARLKNRRNROVCIIDPKLKWIOE 60

OY 61 YLEKALN 67
| | | | |
Db 61 YLEKALN 67

RESULT 5
AAM50760
ID AAM50760 standard; peptide: 67 AA.
XX
AC AAM50760;
XX
DT 27-JUL-1998 (first entry)
XX
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
XX
KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
XX HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
OS Homo sapiens.
XX
PN FR2751658-A1.
XX
PA 30-JAN-1998.
PD
PE 26-JUL-1996; 96FR-0009477.
XX
PR 26-JUL-1996; 96FR-0009477.
XX
PA (INSP) INST PASTEUR.
XX
PA Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL.
PI WPI: 1998-123039/12.
XX
PT Human stromal cell-derived chemokine, SDF-1 - useful for creating
PT human immunodeficiency virus infection
XX
PS Claim 2; Page 29; 48pp; French.

XX The invention relates to peptides which bind to a cellular receptor for
CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC expressed transmembrane domain receptor), especially where the
CC peptide is human chemokine SDF-1. The peptide can be used to treat or
CC prevent HIV infections, optionally together with reverse transcriptase
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
CC receptor antagonists, immunotherapy agents, agents for treating HIV-

CC associated opportunistic infections and/or other CXC or CC chemokines,
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.

XX
 SQ Sequence 67 AA;

Query Match 95.6%; Score 346; DB 19; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 6
 AAY34092
 ID AAY34092 standard; protein; 67 AA.

AC AAY34092;
 XX
 DT 29-NOV-1999 (first entry)

DE Native stromal cell derived factor 1 (SDF-1) alpha protein.

XX CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KM Interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KM angiogenesis; stromal cell derived factor 1; SDF-1.

XX Mammalia.

XX WO9447158-A2.

XX PD 23-SEP-1999.

XX PF 12-MAR-1999; 99WO-CA00221.

XX PR 13-MAR-1998; 98CA-2226391.

XX PR 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Durotojo V;

XX WPI; 1999-561857/47.

XX Use of CXC chemokine receptor 4 for treating autoimmune disease and

XX cancer -

XX Example 1; Fig 1; 71pp; English.

XX The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)
 CC antagonist for the manufacture of a medicament for reducing Interferon
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
 CC to treat or to design a medicament to treat, an autoimmune disease,
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
 CC antagonists may be peptide compounds comprising a substantially purified
 CC peptide fragment, analogue or a pharmacologically acceptable salt of
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents
 CC the amino acid sequence of SDF-1 alpha protein.

XX SQ Sequence 67 AA;

Query Match 95.6%; Score 346; DB 20; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 7
 AAY06741
 ID AAY06741 standard; protein; 67 AA.

AC AAY06741;
 XX

DT 18-JUN-1999 (first entry)

DE SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
 KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;
 KM stromal cell derived factor 1; Macrophage Inflammatory protein.

XX Synthetic.
 OS Homo sapiens.

XX WO911655-A1.

XX PD 11-MAR-1999.

XX PF 31-AUG-1998; 98WO-US18096.

XX PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

XX Kent SBH, Stanl MA, Simon R, Wilken J;

XX WPI; 1999-205128/17.

XX New cross-over proteins for treatment of inflammation and infections
 PT e.g. AIDS - prepared by ligation of two functional protein modules
 derived from two different parent molecules

XX Example 4; Page 43; 75pp; English.

XX The invention relates to a cross-over protein produced by chemical
 CC ligation of at least two functional protein modules derived from at
 CC least two parent protein molecules. The cross-over proteins can be used
 CC in pharmaceutical compositions for therapy of inflammatory and
 CC infectious diseases including AIDS, and for indications of hematopoiesis
 CC and chemoprotection. They are also useful for treatment of asthma,
 CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library
 CC comprising a collection of cross-over proteins is useful for screening
 CC for cross-over proteins that are receptor ligands. The libraries
 CC comprise functionally diverse compounds therefore improving the drug
 CC discovery process. The proteins and libraries are exemplified by the
 CC preparation of cross-over chemokines comprising various combinations of
 CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor
 CC 1), VMP (viral Macrophage Inflammatory protein) and other such
 CC chemokines. Sequences AAY06741-62 represent amino acid sequences of SDF-1
 CC alpha/RANTES cross-over molecules.

XX SQ Sequence 67 AA;

Query Match 95.6%; Score 346; DB 20; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLWIOE 60
 DB 1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLWIOE 60

OY 61 YLEKALN 67
 |||||
 Db 61 YLEKALN 67

RESULT 8
 AAY06726
 ID AAY06726 standard; protein; 67 AA.
 XX
 AC AAY06726;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Amino acid fragment of SDF-1 alpha.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
 KW Infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; vmi;
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;
 KW stromal cell derived factor 1; Macrophage inflammatory protein.
 XX

OS Homo sapiens.
 OS Synthetic.

PN WO9911655-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

PI Kent SBH, Stanl MA, Simon R, Wilken J;

DR WPI: 1999-205128/17.

XX
 PT New cross-over proteins for treatment of inflammation and infections
 PT e.g. AIDS - prepared by ligation of two functional protein modules
 PT derived from two different parent molecules

XX Example 4; Page 41; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical
 CC ligation of at least two functional protein modules derived from at least
 CC two parent protein molecules. The cross-over proteins can be used in
 CC pharmaceutical compositions for therapy of inflammatory and infectious
 CC diseases including AIDS, and for indications of hematopoiesis and
 CC chemoprotection. They are also useful for treatment of asthma, allergic
 CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library
 CC comprising a collection of cross-over proteins is useful for screening
 CC for cross-over proteins that are receptor ligands. The libraries comprise
 CC functionally diverse compounds therefore improving the drug discovery
 CC process. The proteins and libraries are exemplified by the preparation
 CC of cross-over chemokines comprising various combinations of peptide
 CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), vmi
 CC (Viral Macrophage Inflammatory protein) and other such chemokines. The
 CC present sequence represents an amino acid fragment of SDF-1 alpha which
 CC acts as a synthetic base molecule for synthesizing the cross-over
 CC protein.
 XX

XX Sequence 67 AA:

Query Match 95.6%; Score 346; DB 20; Length 67;
 Best local similarity 97.0%; Pred. No. 3.5e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANKVHLKILNTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60
 |||||
 Db 1 KPVSLSYRCPCRFESHVARANKVHLKILNTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60
 OY 61 YLEKALN 67

Db 61 YLEKALN 67
 |||||

RESULT 9
 AAY67594
 ID AAY67594 standard; peptide; 67 AA.
 XX
 AC AAY67594;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE SDF-1alpha peptide sequence.

XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes; ulcerative colitis; lupus; angiotensin; antitumor;
 KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.
 XX

OS Unidentified.

PN WO200009152-A1.

PD 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI: 2000-224175/19.

XX
 PT Therapeutic composition containing CXCR4 antagonist, useful for
 PT treating autoimmune disease, especially multiple sclerosis and cancer

XX Disclosure; Fig 1; 88pp; English.

CC The invention provides a therapeutic composition containing an antagonist
 CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions
 CC are specifically used to reduce production of gamma-interferon by T
 CC cells, particularly for treating autoimmune disease, especially multiple
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
 CC colitis, gout, lupus and transplant rejection; to treat cancer by
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
 CC evaluate in vivo pharmacokinetics, or to determine disease progression
 CC and susceptibility, or as targeting agents for delivery of other
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
 CC derived factor one) peptide fragments, SDF-1 being the only known natural
 CC ligand for CXCR4. The present sequence represents a SDF-1alpha
 CC peptide sequence.
 XX

XX Sequence 67 AA:

Query Match 95.6%; Score 346; DB 21; Length 67;
 Best local similarity 97.0%; Pred. No. 3.5e-38;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANKVHLKILNTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60
 |||||
 Db 1 KPVSLSYRCPCRFESHVARANKVHLKILNTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60
 OY 61 YLEKALN 67
 |||||
 Db 61 YLEKALN 67
 RESULT 10
 AAY47680

```

ID AAB47680 standard; peptide: 67 AA.
XX
AC AAB47680;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1-alpha.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KN macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KM autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Homo sapiens.
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PR 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
XX
PR 14-SEP-2000; 2000US-232425P.
XX
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI: 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation -
XX
PS Claim 8: Page 57; 74pp: English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogeneic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 67 AA:
OY Query Match 95.6%; Score 346; DB 23; Length 67;
DB Best Local Similarity 97.0%; Pred. No. 3..5e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
OY 1 KGVSLPYRPCPCFFESHVARAVKHLKLINTFNCALQIYARLKNRRVCIPDKLKWIOE 60
DB 1 KPVSYLSYRPCCFESHVARAVKHLKLINTFNCALQIYARLKNRRVCIPDKLKWIOE 60
OY YLEKALN 67
DB YLEKALN 67
RESULT 11
1D AAM50761 standard; peptide: 68 AA.
AC AAM50761;
XX

```

[illegible]

OS Homo sapiens.
OS Synthetic.
XX
PM WO9920759-A1.
XX
PD 29-APR-1999.
XX
PF 21-OCT-1998; 98WO-US22282.
XX
PR 20-OCT-1998; 98US-0175713.
PR 22-OCT-1997; 97US-0955826.
PR 27-FEB-1998; 98WO-US04002.
XX
PA (GENY) GENETICS INST INC.
XX
PI Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
PI Yang O;
XX
DR WPI: 1999-288307/24.
DR N-PSDB; AAX25530.
XX
PT Modified chemokines useful for inhibiting or stimulating
PT angiogenesis
XX
PS Claim 6c: Page 79; 85pp; English.
XX
CC The present sequence represents met-hsdf-1 alpha, i.e. human
CC stromal cell derived growth factor-1 alpha having an added
CC N-terminal methionine residue. DNA encoding met-hsdf-1 alpha (see
CC AA25530) was produced by cloning an NdeI/XbaI-restricted hsdF-1
CC alpha PCR product into the E. coli expression vector pAL781
CC in-frame with an ATG codon. met-hsdf-1 alpha is an example of
CC novel N-terminal modified chemokines (see AA05818-21) that have at
CC least one Met residue, at least one aminoxy/penicillamine residue or at
CC least one GroHEK peptide (see AA05822) covalently attached at the
CC C-terminus. The N-terminal modified chemokines are useful for
CC altering receptor function, inhibiting interactions between
CC chemokine receptors and their ligands. They are used as research
CC tools for identifying chemokine receptors, as vaccine adjuvants, as
CC agents for the chemotactic recruitment of migratory cells, as agents
CC for the stimulation or inhibition of angiogenesis, as agents against
CC autoimmune diseases and inflammation, and as agents to inhibit the
CC binding of HIV to certain receptors and the infection of
CC susceptible cells by HIV. HIV infection is best treated with
CC modified SDF-1 alpha and beta or MIP-1 alpha and beta.
XX
SQ Sequence 69 AA:

Query Match 95.6%; Score 346; DB 20; Length 69;
Best Local Similarity 97.0%; Pred. No. 3.7e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 2 KPVSLSYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61
QY 61 YLEKALN 67
DB 62 YLEKALN 68

RESULT 13
AAW50762
ID AAW50762 standard: peptide; 72 AA.
XX
XX AAW50762;
XX
DT 27-JUL-1998 (first entry)
XX
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
XX
XX Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.

XX
OS Homo sapiens.
XX
PM FR2751658-A1.
XX
PD 30-JAN-1998.
XX
PF 26-JUL-1996; 96FR-0009477.
XX
PR 26-JUL-1996; 96FR-0009477.
PR 26-JUL-1996; 96FR-0009477.
XX
PA (INSP) INST PASTEUR.
XX
PI Arenzana SF, Baggiolini M, Clark LT, Moser B, Virelizier JL;
PI WPI: 1998-123039/12.
XX
DR Human stromal cell-derived chemokine, SDF-1 - useful for treating
DR human immunodeficiency virus infection
XX
PT Claim 5; Page 29; 48pp; French.
XX
PS The invention relates to peptides which bind to a cellular receptor for
XX CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
XX expressed transmembrane domain receptor), especially where the
XX peptide is human chemokine SDF-1. The peptide can be used to treat or
XX prevent HIV infections, optionally together with reverse transcriptase
XX inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
XX receptor antagonists, immunotherapy agents, agents for treating HIV-
XX associated opportunistic infections and/or other CXC or CC chemokines,
XX especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be
XX used to detect anti-SDF-1 antibodies in biological fluids. This
XX sequence represents a specifically claimed peptide which binds to the
XX CXCR4 receptor.
XX
SQ Sequence 72 AA:

Query Match 95.6%; Score 346; DB 19; Length 72;
Best Local Similarity 97.0%; Pred. No. 3.9e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KPVSLSYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 14
AAV34093
ID AAV34093 standard: protein; 72 AA.
XX
XX AAV34093;
XX
DT 29-NOV-1999 (first entry)
XX
DE Native stromal cell derived factor 1 (SDF-1) beta protein.
XX
XX CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;
KW angiogenesis; stromal cell derived factor 1; SDF-1.
XX
XX Mammalia.
OS
PM WO9947158-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-CA00221.
XX
PR 13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Clark-Lewis I, Gong J, Duroonio V;
XX WPI; 1999-561857/47.
XX
XX Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and
PT cancer -
XX
XX Example 1: Fig 1; 71pp: English.
XX
XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)
CC antagonist for the manufacture of a medicament for reducing interferon
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
CC to treat or to design a medicament to treat, an autoimmune disease,
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
CC antagonists may be peptide compounds comprising a substantially purified
CC peptide fragment, analogue or a pharmacologically acceptable salt of
CC stromal cell derived factor 1 (SDF-1). The present sequence represents
CC the amino acid sequence of SDF-1 beta protein.
XX
SQ Sequence 72 AA:
Query Match 95.6%; Score 346; DB 20; Length 72;
Best Local Similarity 97.0%; Pred. No. 3.9e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
RESULT 15
AAV67595
ID AAV67595 standard; peptide: 72 AA.
XX
XX AAV67595;
XX
XX 13-JUN-2000 (first entry)
XX
XX SDF-1beta peptide sequence.
XX
XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KM type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;
XX stromal cell derived factor one; anti-inflammatory; immunomodulatory.
XX
XX Unidentified.
XX
XX WO200009152-A1.
XX
XX 24-FEB-2000.
XX
XX 16-AUG-1999; 99WO-CA00750.
XX
XX 14-AUG-1998; 98CA-2245224.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Clark-Lewis I, Gong J, Duroonio V, Salari H;
XX WPI; 2000-224175/19.
XX
XX Therapeutic composition containing CXCR4 antagonist, useful for
PT treating autoimmune disease, especially multiple sclerosis and cancer
PT
XX

PS Disclosure; Fig 1; 88pp; English.
XX
XX The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells, particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1beta
XX peptide sequence.
XX
SQ Sequence 72 AA:
Query Match 95.6%; Score 346; DB 21; Length 72;
Best Local Similarity 97.0%; Pred. No. 3.9e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67

Search completed: January 23, 2003, 15:33:42
Job time : 28.2 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:33:47 : Search time 9.8 seconds
(without alignments)
201.157 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362
Sequence: 1 KGVSLPYRCPCRFESHVAR.....QVCIDPKLKIOWIELEKALN 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	89	1	US-08-323-084A-1
2	346	95.6	89	1	US-08-674-008-1
3	346	95.6	93	1	US-08-323-084A-5
4	346	95.6	93	1	US-08-674-008-5
5	346	95.6	326	3	US-08-808-720-3
6	346	95.6	328	3	US-08-808-720-1
7	345	95.3	79	1	US-08-181-556-2
8	96.5	26.7	99	2	US-08-436-420-25
9	96.5	26.7	99	1	US-08-352-324A-6
10	96.5	26.7	99	2	US-08-862-607-6
11	96.5	26.7	99	2	US-08-468-819-3
12	96.5	26.7	99	3	US-09-203-235-6
13	96.5	26.7	99	4	US-08-679-493A-150
14	96.5	26.7	99	5	PCT-US95-16144-6
15	96.5	26.7	99	6	Sequence 5, Appl 1
16	94.5	26.1	70	1	US-08-330-163-24
17	94.5	26.1	70	1	US-08-482-111-24
18	94	26.0	67	1	US-08-244-702-12
19	94	26.0	67	1	US-08-244-702-14
20	94	26.0	68	1	US-08-244-702-9
21	94	26.0	68	1	US-08-244-702-10
22	94	26.0	68	1	US-08-244-702-11
23	94	26.0	69	1	US-08-244-702-2
24	94	26.0	69	1	US-08-244-702-8
25	94	26.0	72	1	US-07-956-863-1
26	94	26.0	72	1	US-07-778-413E-16
27	94	26.0	72	1	US-08-340-102-16

28	94	26.0	72	1	US-08-330-163-1	Sequence 1, Appl 1
29	94	26.0	72	1	US-08-244-702-1	Sequence 1, Appl 1
30	94	26.0	72	1	US-08-482-111-1	Sequence 1, Appl 1
31	94	26.0	72	1	US-08-202-989-1	Sequence 1, Appl 1
32	94	26.0	72	5	PCT-US94-02051-1	Sequence 1, Appl 1
33	94	26.0	73	1	US-08-482-111-69	Sequence 69, Appl 1
34	94	26.0	73	4	US-09-384-302A-26	Sequence 26, Appl 1
35	94	26.0	76	2	US-08-468-819-79	Sequence 79, Appl 1
36	94	26.0	76	2	US-08-468-819-81	Sequence 81, Appl 1
37	92	25.4	64	1	US-08-330-163-21	Sequence 21, Appl 1
38	92	25.4	64	1	US-08-482-111-21	Sequence 8, Appl 1
39	92	25.4	71	3	US-08-615-232A-8	Sequence 8, Appl 1
40	92	25.4	71	3	US-08-470-323-8	Sequence 8, Appl 1
41	91.5	25.3	72	3	US-08-846-966-1	Sequence 1, Appl 1
42	91.5	25.3	72	3	US-08-557-142-1	Sequence 1, Appl 1
43	91.5	25.3	72	4	US-09-467-160-1	Sequence 1, Appl 1
44	91.5	25.3	72	4	US-09-513-153-1	Sequence 1, Appl 1
45	91.5	25.3	72	4	US-09-467-155-1	Sequence 1, Appl 1

ALIGNMENTS

RESULT 1
US-08-323-084A-1
; Sequence 1, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-1

Query Match 95.6%; Score 346; DB 1; Length 89;

Best local Similarity 97.0%; Pred. No. 7e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILTPNCALDIYARLKNNNQVCIDPKLKIOWIE 60
DB 22 KPVSLPYRCPCRFESHVARANKHLKILTPNCALDIYARLKNNNQVCIDPKLKIOWIE 81
QY 61 YLEKALN 67

Db 82 YLEKALN 88

RESULT 2

US-08-674-008-1
; Sequence 1, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-674-008-1

Query Match 95.6%; Score 346; DB 1; Length 89;
Best Local Similarity 97.0%; Pred. No. 7e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSLPYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNQVCDPRLKIQE 60
Db 22 KPVSLYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNQVCDPRLKIQE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 3

US-08-323-084A-5
; Sequence 5, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-5

Query Match 95.6%; Score 346; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 7.3e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNQVCDPRLKIQE 60
Db 22 KPVSLYRCPCRFESHVARANKHLKILTPNCALQIVARLKNNNQVCDPRLKIQE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 4

US-08-674-008-5
; Sequence 5, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 280505/1993
: FILING DATE: 14-OCT-1993
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)293-7060
: TELEFAX: (202)293-7860
: TELETYPE: 6491103
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 93 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-674-008-5

Query Match 95.6%; Score 346; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 7.3e-38;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCEFFESHVARANVKHLKITLTPNCALQIVARLKNNNROVCIIDPKLKWIOE 60
DB 22 KPVSLSTPCPCFFESHVARANVKHLKITLTPNCALQIVARLKNNNROVCIIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 5
US-08-808-720-3
: Sequence 3, Application US/08808720
: Patent No. 6100387
: GENERAL INFORMATION:
: APPLICANT: Herrmann, Steve
: APPLICANT: Swanberg, Stephen
: TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
: TITLE OF INVENTION: CHEMOKINE DOMAINS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 Cambridgepark
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/808.720
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Sprunger, Suzanne
: REGISTRATION NUMBER: P-41,323
: REFERENCE/DOCKET NUMBER: G15291
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8284
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 326 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-808-720-3

Query Match 95.6%; Score 346; DB 3; Length 326;
Best Local Similarity 97.0%; Pred. No. 3.2e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCEFFESHVARANVKHLKITLTPNCALQIVARLKNNNROVCIIDPKLKWIOE 60
DB 20 KPVSLSTPCPCFFESHVARANVKHLKITLTPNCALQIVARLKNNNROVCIIDPKLKWIOE 79
OY 61 YLEKALN 67
DB 80 YLEKALN 86

RESULT 6
US-08-808-720-1
: Sequence 1, Application US/08808720
: Patent No. 6100387
: GENERAL INFORMATION:
: APPLICANT: Herrmann, Steve
: APPLICANT: Swanberg, Stephen
: TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
: TITLE OF INVENTION: CHEMOKINE DOMAINS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 Cambridgepark
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/808.720
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Sprunger, Suzanne
: REGISTRATION NUMBER: P-41,323
: REFERENCE/DOCKET NUMBER: G15291
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8284
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 328 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-808-720-1

Query Match 95.6%; Score 346; DB 3; Length 328;
Best Local Similarity 97.0%; Pred. No. 3.3e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCEFFESHVARANVKHLKITLTPNCALQIVARLKNNNROVCIIDPKLKWIOE 60
DB 22 KPVSLSTPCPCFFESHVARANVKHLKITLTPNCALQIVARLKNNNROVCIIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 7
US-08-181-556-2
: Sequence 2, Application US/08181556
: Patent No. 5523486
: GENERAL INFORMATION:
: APPLICANT: HONJO, Tasuku
: APPLICANT: TASHIRO, Kei
: APPLICANT: TADA, Hideaki

```

1  TITLE OF INVENTION:  PROCESS FOR CONSTRUCTING CDNA LIBRARY,
2  TITLE OF INVENTION:  AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
3  NUMBER OF SEQUENCES:  11
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  STEVENS, DAVIS, MILLER & MOSHER
6  STREET:  515 No. 5525486th Washington Street (P.O. Box 1427)
7  CITY:  Alexandria
8  STATE:  Virginia
9  COUNTRY:  USA
10 ZIP:  22313
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Floppy disk
14 COMPUTER:  IBM PC compatible
15 OPERATING SYSTEM:  PC-DOS/MS-DOS
16 SOFTWARE:  PatentIn Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER:  US/08/181,556
19 FILING DATE:  14-JAN-1994
20 CLASSIFICATION:  424
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:  JP 5-22098
23 FILING DATE:  14-JAN-1993
24 ATTORNEY/AGENT INFORMATION:
25 NAME:  POULOS III, James A.
26 REGISTRATION NUMBER:  31714
27 REFERENCE/DOCKET NUMBER:  TP/29088
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE:  (703) 549-7200
30 TELEFAX:  (703) 528-5313
31
32 TELEX:  89-2746
33 INFORMATION FOR SEQ ID NO:  2:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH:  89 amino acids
36 TYPE:  amino acid
37 TOPOLOGY:  linear
38
39 MOLECULE TYPE:  protein
40
41 US-08-181-556-2

```

Query Match	95.3%	Score	345	DB	1	Length	89
Best Local Similarity	95.5%	Pred. No.	9.4e-38				
Matches	64	Conservative	1	Mismatches	2	Indels	0
						Gaps	0

	Qy	1	KGSLPRCCRFEEESHVARANVHKILINTPCALQIYARLKNNRQVCIDPKLKWIOE	60
Dd	22	KPSLSLRCCRFEESHIARANVKHKLINTPCALQIYARLKNNRQVCIDPKLKWIOE	81	
	Qy	61	YLEKALN 67	.
Dd	82	YLEKALN 88		

```

1      RESULT 8
2      US-08-436-420-25
3      ; Sequence 25, Application US/08436420
4      ; Patent No. 5840524
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: VAN DAMME, Jo; and
8      ; APPLICANT: PROOST, Paul
9      ;
10     ; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN
11     ;
12     ; NUMBER OF SEQUENCES: 45
13     ;
14     ; CORRESPONDENCE ADDRESS:
15     ; ADDRESSEE: HALE and DORR LLP
16     ; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
17     ; CITY: WASHINGTON
18     ; STATE: DISTRICT OF COLUMBIA
19     ; COUNTRY: USA
20     ;
21     ; ZIP: 20004
22     ;
23     ; COMPUTER READABLE FORM:
24     ; MEDIUM TYPE: Floppy disk
25     ; COMPUTER: IBM PC compatible
26     ; OPERATING SYSTEM: PC-DOS/MS-DOS
27     ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
28     ;
29     ; CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/436,420
FILING DATE: 24-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03330
FILING DATE: 26-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/982,539
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102378.215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 942-8400
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-420-25

Query Match      26.7%   Score 96.5   DB 2:   Length 79;
Best Local Similarity 31.1%   Pred. No.1.8e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

```

		Query Match	Best Local Similarity	Score 96.5; DA 2 31.1%; Pred. No. 1.8e-05;	length 79; Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5
OY	1	KGVSLP-----YRCRC-RFESHVARAVKHLKIINT--PNCA-LDIYATLKNNNOYCID	52		
Dd	1	EGAIVPSRAKETLRCCGCIITYSKRPFHFKFIKLDAIESGFCHCATELIYVL-SDGRCLCID	59		
OY	53	PRLKWIOEYLEKAL	66		
Dd	60	PKENWVQRYVEKEFL	73		

RESULT 9 -
 US-08-352-324A-6
 Sequence 6, Application US/08352324A
 Patent No. 5633149
 GENERAL INFORMATION:
 APPLICANT: Guegler, Karl J.
 APPLICANT: Hawkins, Phillip R.
 APPLICANT: Wilde, Craig G.
 APPLICANT: Sellhammer, Jeffrey J.
 TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
 TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEO Version 1.5
 CURRENT APPLICATION DATA: 1.5
 APPLICATION NUMBER: US/08/352,324A
 FILING DATE: 07-DEC-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Luther, Barbara J.
 REGISTRATION NUMBER: 33,954
 REFERENCE/DOCKET NUMBER: PR-0025 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-352-324A-6

Query Match 26.7%: Score 96.5; DB 1; Length 99;
Best Local Similarity 31.1%: Pred. No. 2.3e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNROVCID 52
DB 21 EGAVLPBSAKELRCQCICKYKSPFHPKFIKELRVIESGPHCANTETIIVKL-SGGRLECID 79
QY 53 PKLKIQETYLEKAL 66
DB 80 PENWQRYVEKFL 93

RESULT 10

US-08-862-607-6
Sequence 6, Application US/08862607
Patent No. 5844084
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Selhammer, Jeffrey J.
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,607
FILING DATE: 23-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-862-607-6

Query Match 26.7%: Score 96.5; DB 2; Length 99;
Best Local Similarity 31.1%: Pred. No. 2.3e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNROVCID 52
DB 21 EGAVLPBSAKELRCQCICKYKSPFHPKFIKELRVIESGPHCANTETIIVKL-SGGRLECID 79
QY 53 PKLKIQETYLEKAL 66
DB 80 PENWQRYVEKFL 93

RESULT 11

US-08-468-819-3
Sequence 3, Application US/08468819
Patent No. 5871723
GENERAL INFORMATION:
APPLICANT: Strieter, Robert M.
APPLICANT: Polverini, Peter J.
APPLICANT: Kunkel, Steven L.
TITLE OF INVENTION: CXc Chemokines as Regulators of
TITLE OF INVENTION: Angiogenesis
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,819
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UMIC:003/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-819-3

Query Match 26.7%: Score 96.5; DB 2; Length 99;
Best Local Similarity 31.1%: Pred. No. 2.3e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNROVCID 52
DB 21 EGAVLPBSAKELRCQCICKYKSPFHPKFIKELRVIESGPHCANTETIIVKL-SGGRLECID 79
QY 53 PKLKIQETYLEKAL 66
DB 80 PENWQRYVEKFL 93

RESULT 12

US-09-203-235-6
Sequence 6, Application US/09203235
Patent No. 6071701
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.

```

; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; TITLE OF INVENTION: INFILAMED ADENOMID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/203,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,607
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-203-235-6

Query Match      26.7% Score 96.5; DB 3; Length 99;
Best Local Similarity 31.1%; Pred.No.2.3e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

Oy      1 KGVSIP-----RCPC-RFFESHVARANKVHKLIINT-PNCA-LQIVARIKNNROVCID 52
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      21 EAVVLPRAKELRCCCIKIYSKPFHFKFIKELRVIESGHCANTEIIVVL-SDGRRLCID 79
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy      53 PKLWIOEYLEKAL 66
       || | | | | | |
Db      80 PKNWVQRVVERKL 93

RESULT 13
; US-08-679-493A-150
; Sequence 150, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ IDS NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 150
; LENGTH: 99

```

```

      : TYPE: PRT
      : ORGANISM: Homo sapiens
US-08-679-493A-150

Query Match
Best Local Similarity 26.7%; Score 96.5; DB 4; Length 99;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

QY 1 KGVSLP-----YRCPC-RFESHVARANKHLKIINT--PNCA-LQIVARLKNNRQVCID 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 21 EGAVLPRAAKELRCCQIKITYSKPFHPKFIKELRVIESGPHCANTEIIYKL--SDGRELCID 79
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 53 PKLWIOEYLEKAL 66
   |||:|||||
Db 80 PKNWVRVERKEFL 93
   |||:|||||

RESULT 14
PCT-US95-16144-6
; Sequence 6, Application PC/TUS9516144
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFAMED
; TITLE OF INVENTION: ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16144
; FILING DATE: 07-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: P-0025 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-16144-6

Query Match
Best Local Similarity 26.7%; Score 96.5; DB 5; Length 99;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

QY 1 KGVSLP-----YRCPC-RFESHVARANKHLKIINT--PNCA-LQIVARLKNNRQVCID 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 21 EGAVLPRAAKELRCCQIKITYSKPFHPKFIKELRVIESGPHCANTEIIYKL--SDGRELCID 79
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 53 PKLWIOEYLEKAL 66
   |||:|||||
Db 80 PKNWVRVERKEFL 93
   |||:|||||

```

```
RESULT 15
5451399-2
; Patent No. 5451399
; APPLICANT: GIMBRINE, MICHAEL A.; OBIN, MARTIN S.; BAKER,
; JOFFRE, B.; HEBERT, CAROLINE A.
; TITLE OF INVENTION: [ALA IL-8]77 AND [SER IL-8]72 AS
; LEUKOCYTE ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/964,525
; FILING DATE: 19-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 443,131
; FILING DATE: 29-NOV-1989
; SEQ ID NO:2:
; LENGTH: 99
5451399-2

Query Match          26.7%; Score 96.5; DB 6; Length 99;
Best Local Similarity 31.1%; Pred No. 2.3e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

Qy 1 KGVSLP-----YRCP-REFESHVARANVHLKILNT-PNCA-LQIVARIKNNNQVCID 52
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 21 ECAVLPRSAKELRCQICKTYSKPFHPKFIKELRVIESGPHCANTEIIVKL-SDGRELCID 79
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 53 PKLKIQOEYLEKAL 66
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 80 KRNWQVRVVEKFL 93
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: January 23, 2003, 15:38:58
Job time : 10.8 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 ; Search time 6.2 Seconds
(without alignments)
218.059 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362
Sequence: 1 KGVSLPYRCRCFFESHVAR.....QVCIDPKLKIQVLEKALN 67

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	67	9	US-09-852-424-3
2	354	97.8	67	9	US-09-852-424-1
3	353	97.5	67	9	US-09-852-424-7
4	349	96.4	67	9	US-09-852-424-6
5	348	96.1	67	9	US-09-852-424-9
6	347	95.9	67	9	US-09-852-424-2
7	347	95.9	67	9	US-09-852-424-5
8	346	95.6	67	9	US-09-852-424-8
9	346	95.6	67	9	US-09-835-107-1
10	346	95.6	67	10	US-09-144-838-8
11	346	95.6	67	10	US-09-144-838-23
12	346	95.6	89	8	US-08-927-939-22
13	346	95.6	89	9	US-09-792-793A-32
14	346	95.6	89	10	US-09-953-692-4
15	346	95.6	89	10	US-09-953-717-4
16	346	95.6	93	8	US-08-927-939-56
17	346	95.6	93	8	US-09-835-107-2
18	346	95.6	93	9	US-09-835-107-3
19	346	95.6	93	9	US-09-792-793A-93

20	346	95.6	93	10	US-09-144-838-7	Sequence 7, Appl
21	346	95.6	93	10	US-09-919-497-95	Sequence 95, Appl
22	346	95.6	320	9	US-09-792-793A-77	Sequence 77, Appl
23	346	95.6	322	9	US-09-792-793A-78	Sequence 78, Appl
24	346	95.6	327	9	US-09-792-793A-79	Sequence 79, Appl
25	344	95.0	67	9	US-09-852-424-4	Sequence 4, Appl
26	339.5	93.8	66	9	US-09-852-424-10	Sequence 10, Appl
27	336.5	93.0	66	9	US-09-852-424-11	Sequence 11, Appl
28	330.5	91.3	66	9	US-09-852-424-12	Sequence 12, Appl
29	328.5	90.7	66	10	US-09-144-838-27	Sequence 27, Appl
30	328.5	88.5	68	10	US-09-144-838-51	Sequence 51, Appl
31	304	84.0	68	10	US-09-144-838-47	Sequence 47, Appl
32	295	81.5	68	10	US-09-144-838-24	Sequence 24, Appl
33	292	80.7	67	10	US-09-144-838-25	Sequence 25, Appl
34	277.5	76.7	67	10	US-09-144-838-28	Sequence 28, Appl
35	269.5	74.4	69	10	US-09-144-838-52	Sequence 52, Appl
36	266.5	73.6	68	10	US-09-144-838-53	Sequence 53, Appl
37	254.5	70.3	68	10	US-09-144-838-29	Sequence 29, Appl
38	253	69.9	68	10	US-09-144-838-48	Sequence 48, Appl
39	250	69.1	67	10	US-09-144-838-49	Sequence 49, Appl
40	241	66.6	68	10	US-09-144-838-26	Sequence 26, Appl
41	223.5	61.7	67	10	US-09-144-838-30	Sequence 30, Appl
42	223	61.6	67	10	US-09-144-838-31	Sequence 31, Appl
43	215.5	59.5	69	10	US-09-144-838-54	Sequence 54, Appl
44	212.5	58.7	66	10	US-09-144-838-35	Sequence 35, Appl
45	199	55.0	68	10	US-09-144-838-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
US-09-852-424-3

Query Match 100.0%; Score 362; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.6e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGVSLPYRCRCFFESHVARANKHLKILNTPCALQIVARLKNRRNRCVCDPKLWQ 60
DB 1 KGVSLPYRCRCFFESHVARANKHLKILNTPCALQIVARLKNRRNRCVCDPKLWQ 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 2
US-09-852-424-1
; Sequence 1, Application US/09852424

```
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; US-09-852-424-1
```

```
Query Match          97.8%; Score 354; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 2,7e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KGVSLLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 1 KGVSLLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
```

```
RESULT 3
US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
```

```
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; US-09-852-424-7
```

```
Query Match          97.5%; Score 353; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 3,4e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KGVSLLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 1 KGVSLLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
```

```
QY 61 YLEKALN 67
Db 61 YLEKALN 67
```

```
RESULT 4
US-09-852-424-6
; Sequence 6, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (5)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; US-09-852-424-6
```

```
Query Match          96.4%; Score 349; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 9,4e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
Db 1 KGVSLLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
```

```
RESULT 5
US-09-852-424-9
; Sequence 9, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (8)
```


OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
OTHER INFORMATION: disclosure for possible structures for P*
OTHER INFORMATION: Description of Artificial Sequence: Engineered in
OTHER INFORMATION: Laboratory
US-09-852-424-9

Query Match 96.1%; Score 348; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.2e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
|||||
Db 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67
|||||
Db 61 VLEKALN 67

RESULT 6
US-09-852-424-2

Sequence 2, Application US/09852424
Patent No. US20020156034A1

GENERAL INFORMATION:

APPLICANT: The University of British Columbia; and

APPLICANT: Chemokine Therapeutics Corporation

TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS

FILE REFERENCE: 80021-257

CURRENT APPLICATION NUMBER: US/09/852,424

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: CA 2,305,787

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US 60/205,467

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 67

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Engineered in

OTHER INFORMATION: Laboratory
US-09-852-424-2

Query Match

Best Local Similarity 95.9%; Score 347; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.6e-31;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
|||||
Db 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67
|||||
Db 61 VLEKALN 67

RESULT 7
US-09-852-424-5

Sequence 5, Application US/09852424
Patent No. US20020156034A1

GENERAL INFORMATION:

APPLICANT: The University of British Columbia; and

APPLICANT: Chemokine Therapeutics Corporation

TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS

FILE REFERENCE: 80021-257

CURRENT APPLICATION NUMBER: US/09/852,424

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: CA 2,305,787

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US 60/205,467

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5

LENGTH: 67

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Engineered in

OTHER INFORMATION: Laboratory
US-09-852-424-5

Query Match 95.9%; Score 347; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.6e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
|||||
Db 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67
|||||
Db 61 VLEKALN 67

RESULT 8
US-09-852-424-8

Sequence 8, Application US/09852424
Patent No. US20020156034A1

GENERAL INFORMATION:

APPLICANT: The University of British Columbia; and

APPLICANT: Chemokine Therapeutics Corporation

TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS

FILE REFERENCE: 80021-257

CURRENT APPLICATION NUMBER: US/09/852,424

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: CA 2,305,787

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US 60/205,467

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 67

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: MUTAGEN

LOCATION: (7)

OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of

OTHER INFORMATION: disclosure for possible structures for P*

OTHER INFORMATION: Description of Artificial Sequence: Engineered in

OTHER INFORMATION: Laboratory
US-09-852-424-8

Query Match 95.6%; Score 346; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 2e-31;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60
|||||
Db 1 KGVSLPYRCPCRFESHVARAVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67
|||||
Db 61 VLEKALN 67

RESULT 9
US-09-835-107-1

Sequence 1, Application US/09835107
Patent No. US20020156123A1

GENERAL INFORMATION:

APPLICANT: Tudan, Christopher R.

```

: APPLICANT: Merzouk, Ahmed
: APPLICANT: Arab, Lakhdar
: APPLICANT: Saxena, Geeta
: APPLICANT: Eaves, Connie J.
: APPLICANT: Cashman, Johanne
: APPLICANT: Clark-Lewis
: APPLICANT: Salari, Hassan
: TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
: FILE REFERENCE: SMAR012
: CURRENT APPLICATION NUMBER: US/09/835,107
: CURRENT FILING DATE: 2001-08-20
: PRIOR APPLICATION NUMBER: CA 2,305,036
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/232,425
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: CA 2,335,109
: PRIOR FILING DATE: 2001-02-23
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: : LENGTH: 67
: TYPE: prt
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: SDF-1 alpha
: US-09-835-107-1

```

Query Match	95.6%	Score 346;	DB 9;	Length 67;
Best Local Similarity	97.0%	Pred. No. 2e-31;		
Matches 65; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	1 KGVSLPRPCPCRFESHVARAVKHLKLINTPNCALQIYARLKNNNRQVCIDPKLKWIOE	60		
Dd	1 KPVSLTPRCPCRFESHVARAVKHLLKLTNPNCALQIYARLKNNNRQVCIDPKLKWIOE	60		
OY	61 YLEKALN 67			
Dd	61 YLEKALN 67			

```

RESULT 10
US-09-144-838-8
: Sequence 8, Application US/09144838A
: Patent No. US20020051996a1
: GENERAL INFORMATION:
: APPLICANT: Siani, Michael A.
: APPLICANT: Wilken, Jill
: APPLICANT: Simon, Reyna
: APPLICANT: Kent, Stephen B.H.
: TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
: FILE REFERENCE: GREN-020/01US
: CURRENT APPLICATION NUMBER: US/09/144,838A
: CURRENT FILING DATE: 1998-08-31
: EARLIER APPLICATION NUMBER: US 60/057,620
: EARLIER FILING DATE: 1997-09-04
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 8
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8

```

Query Match	95.6%	Score 34.6	DB 10	length 67
Best Local Similarity	97.0%	Pred. No. 2e-31		
Matches	65	Conservative	0	Mismatches 2; Indels 0; Gaps 0
QY	1	KGVSLPYRCPCEFFESHVARAVYKHLKLTINPNCALQIYARLKNNNROYCIDPKLKTIOE	60	
	1			
	1			
bb	1	KPVSLSYRCPCEFFESHVARAVYKHLKLTINPNCALQIYARLKNNNROYCIDPKLKTIOE	60	

Qy	61	YLEKALN	67
		↑↑↑↑↑↑	
Db	61	YLEKALN	67

```

; RESULT 11
; US-09-144-838-23
; Sequence 23, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
; APPLICANT: Stani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GREN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: US 60/057,620
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-144-838-23

```

[illegible]

```

RESULT 12
US-08-927-939--22
; Sequence 22, Application US/08927939
; Patent No. US20010006540A1
; GENERAL INFORMATION:
; APPLICANT: Graininger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022051
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ. ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939--22

```

[illegible]

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds

(without alignments)
355.259 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362
Sequence: 1 KGVSLPRRCPCRFESHVAR.....QVCIDPKKMKIOEYLEKALN 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_73:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	93	2	G01540
2	345	95.3	89	2	A53497
3	345	95.3	89	2	I53416
4	345	95.3	93	2	I81182
5	101	27.9	101	2	I48148
6	97	26.8	95	2	JN0841
7	96.5	26.7	99	2	A37034
8	92	23.4	101	2	S42496
9	92	23.4	120	2	I48147
10	91.5	23.3	96	2	A32954
11	91	23.1	91	1	A46539
12	91	25.1	103	2	A53096
13	89	24.6	120	2	J60177
14	89	24.6	148	1	A30209
15	89	24.6	148	1	S07723
16	87.5	24.2	96	2	JN0572
17	87	24.0	101	2	I46871
18	86	23.8	91	1	A28815
19	84.5	23.3	100	2	JH0200
20	83.5	23.1	92	2	I53322
21	82.5	22.8	75	2	A54188
22	81.5	22.5	75	2	B54188
23	81.5	22.5	119	2	S42881
24	80.5	22.2	96	2	I48099
25	80	22.1	109	2	A54678
26	79.5	22.0	100	2	S21467
27	79.5	22.0	100	2	I55614
28	79.5	22.0	107	2	B38290
29	78.5	21.7	107	2	A28414

ALIGNMENTS

30	78.5	21.7	132	2	A57325	C-X-C chemokine LI
31	78	21.5	96	2	JC2478	ectaxin precursor
32	77.5	21.4	101	2	B28414	growth-regulated p
33	77.5	21.4	114	2	A55010	neutrophil-activat
34	77.5	21.4	117	2	B44253	alveolar macrophag
35	76.5	21.1	103	2	A26736	transformation-ind
36	76.5	21.1	103	2	I50417	RSV-induced protei
37	75.5	20.9	870	2	A41130	dysostrophin homol
38	74	20.4	125	2	I46857	monocyte chemoatr
39	73.5	20.3	107	2	JH0281	macrophage inflamm
40	73	20.2	92	2	A32393	macrophage inflamm
41	72.5	20.0	126	2	A35766	platelet factor 4,
42	71.5	19.8	128	1	TCGU	beta-thromboglobul
43	71	19.6	99	2	JC5295	monocyte chemoatr
44	70.5	19.5	53	2	I64831	gene KC protein -
45	69.5	19.2	104	1	PFH04A	platelet factor 4

RESULT 1
G01540
cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C:Accession: G01540
R:Spotila, L.D.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07697
A:Accession: G01540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <SPO>
A:Cross-references: EMBL:016752; NID:q1272194; PID:9571508
C:Superfamily: beta-thromboglobulin

Query Match 95.6% Score 346; DB 2; Length 93;
Best Local Similarity 97.0% Pred. No. 4.5e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPRRCRFESHVARVANKHLKLTNPNCALQIVARLKNNNRQVCIDPKKMKIOE 60
DB 22 KGVSLPRRCRFESHVARVANKHLKLTNPNCALQIVARLKNNNRQVCIDPKKMKIOE 81

QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C:Accession: A53497; I59582
R:Nagesawa, T.; Kikutan, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-references: GB:D21072; NID:9413905; PID:NBA04648.1; PID:9468457
R:Tashiro, K.; Tada, H.; Heliker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me
A:Reference number: I59582; MUID:93542488; PMID:8342023
A:Accession: I59582
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>

A:Cross-references: GB:L12029; NID:g393179; PIDN:AAA40100.1; PID:g393180
C:Genetics:
A:Gene: SDF-1-alpha
C:Superfamily: beta-thromboglobulin
C:Keywords: cytokine

Query Match 95.3%; Score 345; DB 2; Length 89;
Best Local Similarity 95.5%; Pred. No. 5.7e-35;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3

Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53416
R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A:Title: Molecular cloning of TPRL, a gene whose expression is repressed by the tumor
A:Reference number: I53416; MUID:95073437; PMID:7982471
A:Accession: I53416
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A:Cross-references: GB:S74318; NID:g786393; PIDN:AA32650.1; PID:g786394
C:Genetics:
A:Gene: TPRL
C:Superfamily: beta-thromboglobulin

Query Match 95.3%; Score 345; DB 2; Length 89;
Best Local Similarity 95.5%; Pred. No. 5.7e-35;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 4

cytokine - mouse

C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I81182
R:Tashiro, K.; Tada, H.; Heiker, R.; Shirazu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I81182
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-93 <RES>
A:Cross-references: GB:L12030; NID:g393181; PIDN:AAA40101.1; PID:g393182
C:Genetics:
A:Gene: SDF-1-beta
C:Superfamily: beta-thromboglobulin

Query Match 95.3%; Score 345; DB 2; Length 93;
Best Local Similarity 95.5%; Pred. No. 6e-35;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 5

I48148
Neutrophil attractant protein-1 - guinea pig

C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: I48148
R:Yoshimura, T.; Johnson, D.G.
J. Immunol. 151, 6225-6236, 1993
A:Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (N
A:Reference number: I48148; MUID:94065176; PMID:7504015
A:Accession: I48148
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-101 <RES>
A:Cross-references: GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765
C:Genetics:
A:Gene: NAP-1
C:Superfamily: beta-thromboglobulin

Query Match 27.9%; Score 101; DB 2; Length 101;
Best Local Similarity 35.9%; Pred. No. 4e-05;
Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

QY 8 RCPCRFESHVARANV--VKHLKILNTPNCA-LQIVARLKNNNRQVCIDPKLKWIOEYL 62
DB 33 RCQC--IKHTTTPHFKFKELKLVIESGPCANSEIIVKL-SNRQCLDPPKKKVVQDVV 89

QY 63 EKAL 66
DB 90 SMFL 93

RESULT 6

JN0841
Interleukin-8 - dog

C:Species: Canis lupus familiaris (dog)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995
C:Accession: JN0841
R:Ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
Gene 131, 305-306, 1993
A:Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene
A:Reference number: JN0841; MUID:94010328; PMID:7916715
A:Accession: JN0841
A:Molecule type: DNA
A:Residues: 1-95 <ISH>
A:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is i
C:Genetics:
A:Introns: 22/1: 67/2
C:Superfamily: beta-thromboglobulin

Query Match 26.8%; Score 97; DB 2; Length 95;
Best Local Similarity 34.8%; Pred. No. 0.00012;
Matches 23; Conservative 15; Mismatches 20; Indels 8; Gaps 4;

QY 3 VSLPYRCPCRFESHVARANVHKILNTPNCA-LQIVARLKNNNRQVCIDPKLKW 57
DB 28 VSELRCQC--IKHTSTPHPKYIKELRVYDSGPCENSEIIVKFNNGN-EVCLDPKEKM 84

QY 58 IOEYLE 63
DB 85 VQKVVQ 90


```

A:Molecule type: mRNA
A:Residues: 1-99 <RE2>
A:Cross-references: GB:M17017; NID:g179579; PIDN:AAA35611.1; PID:g179580
R:Kusner, D.J.; Luebberts, E.L.; Nowinski, R.J.; Komieczkowski, M.; King, C.H.; Sedor, J
Kidney Int. 39, 1240-1248, 1991
A>Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells
A:Reference number: 137902; MUID:91374977; PMID:1895676
A:Accession: 137902
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-97 <RE3>
A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA7745.1; PID:g33959
R:Ailouani, S.; Gaetner, H.F.; Mermod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; P
Eur. J. Biochem. 227, 328-334, 1995
A>Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at t
A:Reference number: S67519; MUID:95154308; PMID:7851404
A:Accession: S67519
A:Molecule type: mRNA
A:Residues: 1-99 <ALO>
C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes
C:Comment: This protein is variably processed at the amino end. The major form differs i
C:Genetics:
A:Gene: GDB:IL8
A:Cross-references: GDB:I20099; OMIM:146930
A:Map position: 4q13-q421
A:Introns: 22/1; 67/2; 95/2
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation
F:1-20/Domains: signal sequence #status predicted <SIG>
F:21-99/Product: interleukin-8, minor form #status experimental <MATRA>
F:23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MATE
F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen

Query Match          26.7%; Score 96.5; DB 2; Length 99;
Best Local Similarity 31.1%; Pred. No. 0.00014;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

Oy      1 KGVSIP-----YRCG-C-RFESHVARANVKHLIINT-PNCA-LDIYARLKNNRQVCID 52
       .| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      21 EGAVLPFRSAKELCCICITKYSPKPFHPIKELRVIESGPCAMTEIIIVKL-SDGRRLCID 79
       || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      53 PLKWIOEYLEKAL 66
       || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      80 PKENNVQRVVEKFL 93

RESULT 8
S42496
Interleukin-8 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text-change 19-Jan-2001
C:Accession: S42496; I46997
R:Leestaelels, I.; Greenlund, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.
Submitted to the EMBL Data Library, March 1994
A>Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain re
A:Reference number: S42496
A:Accession: S42496
A:Molecule type: mRNA
A:Residues: 1-101 <LEG>
A:Cross-references: EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254
R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Golditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A>Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine interl
A:Reference number: I46997; MUID:95137691; PMID:7835984
A:Accession: I46997
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-101 <SCDO>
A:Cross-references: GB:S74436; NID:g786590; PIDN:AAB33241.1; PID:g786591
C:Genetics:
A:Gene: IL-8
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation

```

```

F:1-20/Domains signal sequence #status predicted <SIG>
F:21-101/Product: interleukin-8 #status predicted <MAT>

Query Match          25.4%; Score 92; DB 2; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00051;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

OY 3 VSLPRRCRCFFESHVAAN---VKHLKILNT-PNCA-LQIVARLKNNNRQVCIIDPKLKW 57
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 28 MSTLRKCC--IKTHSTPFHKFKELKLVIESGPCENSEITVRL-TNGKEVCADPKREKW 84
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 58 IQEYLEKAL 66
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 VQKVVQAFLL 93

RESULT 9
148147
monocyte chemoattractant protein-1 - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48147
R:Yoshimura, T.
R:Immunol. 150, 5025-5032, 1993
A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression
A:Reference number: I48147; MUID:93267104; PMID:8496603
A:Accession: I48147
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-120 <RES>
A:Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C:Genetics:
A:Gene: MCP-1
C:Superfamily: macrophage inflammatory protein

Query Match          25.4%; Score 92; DB 2; Length 120;
Best Local Similarity 31.7%; Pred. No. 0.00061;
Matches 20; Conservative 11; Mismatches 30; Indels 2; Gaps 2;

OY 2 GVSLEPRRCRCFFESHVAANVKKHLKITLPNCALQIVARLKNNNRQVCIIDPKLKIQEY 61
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 27 GVNP-TC-CYTFPKQIPLKRVKGYERTSSRCQGEAVIFPTLTKKEVCADPTQKWQDY 84
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 62 LEK 64
      :|
Db 85 IAK 87

RESULT 10
A32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1999
A:Accession: A32954; JH0081
R:Quenodo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro
A:Reference number: A32954; MUID:89139485; PMID:2917992
A:Accession: A32954
A:Molecule type: mRNA
A:Residues: 1-96 <OQ>
A:Cross-references: GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043
R:Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou
A:Reference number: JH0081; MUID:89078502; PMID:2909392
A:Molecule type: mRNA
A:Residues: 1-96 <RYS>
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C:Genetics:
A:Map position: 5

```



```
OY      3 VSLPRCCRFEEF-HVARRNVKHLKLINLPNCALQIVARLKNNNNOVCIDPKLEIOEY 61
        | | | : : : | | | | | | | | | | | | | | | | | | | | | |
Db      31 VNFSSTCKLKYEVPRLRLVGGRKAL--NCHLPAIIIFVIKRNNECVTNINDMDVOEX 87
```

RESULT 14

PDGF-inducible JE glycoprotein precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A30209; A44771; A30861
R.Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
A.Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor
A.Reference number: A30209; MUID:88234501; PMID:3287374
A.Accession: A30209
A.Molecule type: DNA

A:Residues: 1-148 <R05>
A:Cross-references: GB:M19681; NID:g193486; PIDN:AAA37684.1; PID:g387168; GB:M19682
R:Kawahara, R. S.; Deuel, T. F.
J. Biol. Chem. 264, 679-682, 1989
A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of smad
A:Reference number: A44771, MUID:89093129, PMID:2910858
A:Accession: A44771
A:Molecule type: DNA; mRNA
A:Residues: 1-148 <KKA2>
A:Cross-references: GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:g387169
[:Genetics:

A: Introns: 26/1; 65/2
C: Superfamily: macrophage inflammatory protein
C: Keywords: cytokine; glycoprotein
F: 12/ Binding site: carboxylate (asn) (covalent) #status predicted

Query Match	24.6%	Score	89	DB	1	Length	148
Best Local Similarity	26.2%	Pred. No.	0.0018				
Matches	16	Conservative	14	Mismatches	31	Indels	0
						Gaps	0

```
Qy      3  VSLPRCPCRFESHVARANVKHLKILNTPCALQIVARLKNRNRVCIDPKLKWIOEYL 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      28  VNAPLTCCYSFSTSKMIPMSRLESXKRITSSRCPKAEAVFVTKLKREVCADPKKEWQTYI 87
```

QY	63	E	63
Dlb	88	K	88

RESULT 15

S07723

Immediate-early serum-responsive protein JE precursor
N/Alternate names: monocyte chemoattractant protein-1

Cispecies: *Rattus norvegicus* (Norway rat)
CIdate: 10-Sep-1999 #sequence 10-Sep-1999 #text_change 10-Sep-1999
CAccession: G07723.1 NM0129

C. Accession: 507/23, ONV120
R; Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18: 23-34, 1990

A:Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential for transcriptional activation

A;Accession: S07723
A;molecule type: DN

A:Residues: 1-148 <TIM>
A:Cross-references: EMBL:X17053; NID:g55530; PIDN:CAA34901.1; PID:g55531b

R; Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991

A: Reference number: JN0128; MWID:91128376; PMID:1704226
A:Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its expression in macrophages
A:Accession: U0139

A;Accession: J01426
A;Molecule type: mRNA

A:Residues: 1-148 <YOS>
A:Cross-references: GB:M57441; NID:g205333; PID:AAA63496.1; PID:g205334
A:Experimental source: spleen cells
A:Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 63
C:Genetics:

A; Introns: 26/1; 65/2
C; Superfamily: macrophage inflammatory protein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

Query Match	24.6%	Score 89	DB 1	Length 148
Best Local Similarity	24.2%	Pred. NO. 0.0018		
Matches 15; Conservative	16;	Mismatches 31;	Indels 0;	Gaps 0

```

0y  - 3 VSLPRCPREEHVAVANVKKHLINTPCALQIVARLKNRNVCCIDPKLKWIOEYL 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  28 VNAPLTCCYSTFGKMLPMSRLNENKRTTSSRCPKAEVYFVTKLREICADPNKEWQKI 87

```

QY	63	EK	64
		1	
Db	88	RK	89

Search completed: January 23, 2003, 15:37:24
Job time : 11.6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 : Search time 6 seconds

(without alignments)
463.152 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362

Sequence: 1 KGVSLPYRCPCRFESHVAR.....QVCIDPKLKWIOEYLEKALN 67

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	93	1	SDF1_FELCA
2	346	95.6	93	1	SDF1_HUMAN
3	345	95.3	89	1	SDF1_MOUSE
4	101	27.9	101	1	IL8_MOUSE
5	100	27.6	101	1	IL8_CAVPO
6	97	26.8	101	1	IL8_CANFA
7	96.5	26.7	99	1	IL8_FELCA
8	93.5	25.8	101	1	IL8_HUMAN
9	92	25.4	101	1	IL8_MACMU
10	92	25.4	120	1	IL8_SHEEP
11	91.5	25.3	96	1	SV02_CAVPO
12	91	25.1	91	1	GRO_MOUSE
13	91	25.1	92	1	SV05_MOUSE
14	91	25.1	103	1	IL8_PIG
15	89.5	24.7	101	1	IL8_CERTO
16	89	24.6	101	1	IL8_BOVIN
17	89	24.6	130	1	SZ05_RAT
18	89	24.6	148	1	SV02_MOUSE
19	88	24.3	91	1	SV02_RAT
20	88	24.3	100	1	SV05_CAVPO
21	88	24.3	120	1	SV16_HUMAN
22	87.5	24.2	96	1	GRO_RAT
23	87	24.0	101	1	IL8_RABIT
24	86	23.8	91	1	SV05_HUMAN
25	86	23.8	119	1	SV24_MOUSE
26	85.5	23.6	50	1	SV05_PIG
27	84.5	23.3	100	1	MP2_MOUSE
28	83.5	23.1	92	1	SV03_RAT
29	82.5	22.8	98	1	SV13_HUMAN
30	82.5	22.8	114	1	SZ06_HUMAN
31	81.5	22.5	71	1	GRO1_RABIT
32	81.5	22.5	112	1	SZ06_BOVIN
33	81.5	22.5	119	1	SZ07_PIG

ALIGNMENTS

RESULT 1	ID	SDP1_FELCA	STANDARD:	PRT:	93 AA.
AC	062657	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).				
GN	SDF1.				
OS	Felis silvestris catus (Cat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
OX	NCBI_Taxid:9685;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Thymus;				
RA	MEDLINE=98450506; PubMed=9777331;				
RA	Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,				
RA	Cal J.S., Sato E., Kohmoto M., Mikami T.;				
RT	"Molecular cloning and sequencing of feline stromal cell-derived				
RT	factor-1 alpha and beta.";				
RL	Eur. J. Immunogenet. 25:303-305(1998).				
CC	- FUNCTION: CHEMOKINE-INDUCED T-LYMPHOCYTES, MONOCYTES, BUT				
CC	NOT NEUTROPHILS.				
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA AND BETA (SHOWN HERE);				
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE				
CC	C-X-C) (CHEMOKINE CXK).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: AB011966; BAA28602.1; -				
DR	HSSP: P48061; ISDF				
DR	InterPro: IPR001089; CXK_cmkline_sm1.				
DR	InterPro: IPR001811; Chemokine_IL8.				
DR	Pfam: PF00048; IL8; 1.				
DR	SMART: SM00199; SCY; 1.				
DR	PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.				
KW	Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.				
FT	SIGNAL	1	19	POTENTIAL	
FT	CHAIN	1	93	STROMAL CELL-DERIVED FACTOR 1.	
FT	DISULFID	30	55	BY SIMILARITY.	
FT	DISULFID	32	71	BY SIMILARITY.	
FT	VARSPLIC	90	93	MISSING (IN ISOFORM ALPHA).	
SEQ	SEQUENCE	93 AA;	10581 MM;	44FC763711E9BE7 CRC64;	

Query Match 95.6%; Score 346; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 1; 1e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 KVSLSRPCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 60
DB 22 KPSLSYRCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 2
SDFL_HUMAN STANDARD: PRT: 93 AA.
AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSE) (HIRH).
GN SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Spotted L.D.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=96039262; PubMed=7490086;
RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
RA Shinohara T., Honjo T.;
RT "Structure and chromosomal localization of the human stromal cell-
RT derived factor 1 (SDF1) gene.";
RL Genomics 28:495-500(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Liver;
RA Begun N.A., Barnard G.F.;
RT "Nucleotide sequence of hIRH, human Interline reduced in
RT hepatomas.";
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RN STRUCTURE BY NMR OF 22-88.
RX MEDLINE=98046030; PubMed=9384579;
RA Crump M.P., Gong J.H., Loetscher P., Rajarathnam K., Amara A.,
RA Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
RA Clark-Lewis I.;
RT "Solution structure and basis for functional activity of stromal
RT cell-derived factor-1, dissociation of CXCR4 activation from binding
RT and inhibition of HIV-1.";
RL EMBO J. 16:6996-7007(1997).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RX MEDLINE=98284037; PubMed=9618518;
RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Stani M.A.,
RA Lolis E.;
RT "Crystal structure of chemically synthesized [N33A] stromal
RT cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT coreceptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
CC -1- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: U16752; AAA97434.1; -
DR EMBL: L36033; AAB39333.1; -
DR EMBL: L36034; AAB39333.1; -
DR EMBL: U19495; AAB40516.1; -
DR PDB: 1SDF; 28-JAN-98.
DR PDB: 2SDF; 17-JUN-98.
DR PDB: 1A15; 12-AUG-98.
DR Genew: HNCN:10672; SDF1.
DR MTM: 600835; -.
DR InterPro: IPR001089; CXK_cmkline_sml1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR POSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 55
FT DISULFID 32 71
FT VSAPLIC 90 93 MISSING (IN ISOFORM ALPHA).
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44EBD CRC64;

Query Match 95.6%; Score 346; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 1; Ie-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVSLSRPCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 60
DB 22 KPSLSYRCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3
SDFL_MOUSE STANDARD: PRT: 89 AA.
AC P40224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSE) (12-O-tetradecanoylphorbol 13-
DE acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE factor) (TUSF).
GN SDF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=94181581; PubMed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=93342488; PubMed=8342023;
RA Tashiro K., Tada H., Heikler R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and
RT type I membrane proteins.";
RL Science 261:600-603(1993).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=95073497; PubMed=7982471;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

```

RA Weinstein I.B.:
 RT "Molecular cloning of TPAPL, a gene whose expression is repressed by
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."
 RL Exp. Cell Res. 215:284-293(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AK/RJ:
 RA Nomura M., Nakata Y., Uzuwa A., Nose M., Akashi M., Suzuki G.:
 RL Submitted (DEC-1994) to the EMBL/Genbank/DDJ databases.
 CC -1- FUNCTION: CHEMOTACTICALLY ACTIVE ON T-LIMPHOCYTES, MONOCYTES, BUT
 NOT NEUTROPHILS.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
 PRECURSOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
 CC ALTERNATIVE CELL-DEPENDENT B-CELL CLONE DM34 CELLS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA AND BETA (SHOWN HERE):
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D21072; BAA04648.1; -
 DR EMBL: L12029; AAA40100.1; -
 DR EMBL: L12030; AAA40101.1; -
 DR EMBL: S74318; AAB32650.1; -
 DR EMBL: D43804; BAA07862.1; -
 DR EMBL: D43805; BAA07863.1; -
 DR PIR: A53497; A53497.
 DR HSSP: P48061; ISDF.
 DR MGD: MGI:103556; Sdfl.
 DR InterPro: IPR001089; CXCL_chmkline_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PR00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 DR CytoKline: Chemotaxis; Growth factor; Signal; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.
 FT DISULFID 30 55
 FT DISULFID 32 71 BY SIMILARITY.
 FT VARSPLIC 89 89 K -> KRLKM (IN ISOFORM BETA).
 SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;
 Query Match 95.3%; Score 345; DB 1; Length 89;
 Best Local Similarity 95.5%; Pred. No. 1.4e-35;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSLPRCPGRFFESHVARANKHLILNTPGALQIVARLKNNNROYCIDPKLWIOE 60
 DB 22 KPVSLRCPGRFFESHVARANKHLILNTPGALQIVARLKNNNROYCIDPKLWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88
 RESULT 4
 IL8_CANPO STANDARD; PRT; 101 AA.
 AC P49113;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein
 1) (NAP-1).
 GN IL8.
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=94065176; PubMed=7504015;
 RA Yoshimura T., Johnson D.G.:
 RT "CDNA cloning and expression of guinea pig neutrophil attractant
 protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig."
 RL J. Immunol. 151:6225-6236(1993).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: L04986; AAA37049.1; -
 DR HSSP: P10145; 2IL8.
 DR InterPro: IPR001089; CXCL_chmkline_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PR00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR CytoKline: Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 101 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;
 Query Match 27.9%; Score 101; DB 1; Length 101;
 Best Local Similarity 35.9%; Pred. No. 1.3e-05;
 Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;
 QY 8 RCPGRFFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNNROYCIDPKLWIOEYL 62
 DB 33 RQCC--IKIHPPHFKFTELKVISSGPCANSEILVKL-SNRQCLDPPKKKWQDVY 89
 QY 63 EKAL 66
 DB 90 SMFL 93
 RESULT 5
 IL8_CANFA STANDARD; PRT; 101 AA.
 AC P41324;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010328; PubMed=7916715;
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.:
 RT "Cloning of a canine gene homologous to the human

RT Interleukin-8-encoding gene.";
 RL Gene 131:305-306(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=95127913; PubMed=7827282;
 RA Matsumoto T., Mohamed A., Onodera T., Kato H., Ohashi T.,
 RA Gotsuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshinara K.,
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;
 RT "Molecular cloning and expression of canine interleukin 8 cDNA.";
 RL Cytokine 6:455-461(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mongrel; TISSUE=Jugular vein;
 RX MEDLINE=95114148; PubMed=7814650;
 RA Kikileka G.L., Smith W.C., Larosa G.J., Manning A.M.,
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,
 RA Michael L.H., Rot A., Entman M.L.;
 RT "Interleukin-8 gene induction in the myocardium after ischemia and
 RT reperfusion in vivo.";
 RL J. Clin. Invest. 95:89-103(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beagle;
 RX MEDLINE=97230298; PubMed=9119462;
 RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;
 RT "Morrelia burgdorferi migrates into joint capsules and causes an up-
 RT regulation of interleukin-8 in synovial membranes of dogs
 RT experimentally infected with ticks.";
 RL Infect. Immun. 65:1273-1285(1997).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D28772; BAA05961.1; -;
 DR EMBL: D14285; BAA03246.1; -;
 DR EMBL: U10308; AAC48434.1; -;
 DR EMBL: AF048717; AAC05134.1; -;
 DR HSSP: P10145; 1IKM.
 DR InterPro: IPR001089; CXCL_Chemokine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTRKXC.
 DR SMART: SM00471; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 101 BY SIMILARITY.
 FT DISULFID 34 61 INTERLEUKIN-8.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;

Query Match 27.6%; Score 100; DB 1; Length 101;
 Best Local Similarity 36.1%; Pred. No. 1.7e-05;
 Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;

OY 3 VSUPLRCPGRFESHVAVANKHLKILNT----PNCALQIVARLKNNNQVCIDPKLKW 57
 DB 28 VSSLRQCQ--IKTHSPFPHKTIKELVIDSGPHCENSELIVKLVNGN-EVCLDPKRW 84

OY 58 IQE----YLEKA 65
 DB 85 VQKVQIFLKKA 96

RESULT 6
 ID IL8_FELICA STANDARD; PRT; 101 AA.
 AC Q9XSX5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straubinger A.F., Simpson K.W., Straubinger R.K.;
 RT "Feline interleukin-8 mRNA.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF158598; AAD40323.1; -;
 DR HSSP: P10145; 1IKM.
 DR InterPro: IPR001089; CXCL_Chemokine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTRKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 101 BY SIMILARITY.
 FT DISULFID 34 61 INTERLEUKIN-8.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;

Query Match 26.8%; Score 97; DB 1; Length 101;
 Best Local Similarity 33.3%; Pred. No. 4.1e-05;
 Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSUPLRCPGRFESHVAVAN---VKHLKILNT-PNCALQIVARLKNNNQVCIDPKLKW 57
 DB 28 ISSLRQCQ--IKTHSPFPHKTIKELVIDSGPHCENSELIVKLVNGKEVCIDPKRW 84
 OY 58 IQEYLE 63
 DB 85 VQKVVE 90

RESULT 7
 ID IL8_HUMAN STANDARD; PRT; 99 AA.
 AC P10145; Q9C077; Q96RG6;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil
 DE chemotactic factor) (MDC8) (T-cell chemotactic factor) (Neutrophil-
 DE activating protein 1) (NAF-1) (Lymphocyte-derived neutrophil-
 DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emoctakin).
 GN IL8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88258376; PubMed-3260265;
 RA Matsushima K., Morishita K., Yoshimura T., Lavi S., Kobayashi Y.,
 RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic
 RT factor (MDC8) and the induction of MDC8 mRNA by Interleukin 1 and
 RT tumor necrosis factor.";
 RL J. Exp. Med. 167:1883-1893(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87224164; PubMed-2953813;
 RA Schmid J., Weissmann C.;
 RT "Induction of mRNA for a serine protease and a
 RT beta-thromboglobulin-like protein in mitogen-stimulated human
 RT leukocytes.";
 RL J. Immunol. 139:250-256(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89313739; PubMed-2664463;
 RA Kowalski J., Denhardt D.T.;
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating
 RT peptide in differentiating HL60 promyelocytes.";
 RL Mol. Cell. Biol. 9:1946-1957(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89309826; PubMed-263993;
 RA Mukaida N., Shitoo M., Matsushima K.;
 RT "Genomic structure of the human monocyte-derived neutrophil
 RT chemotactic factor IL-8.";
 RL J. Immunol. 143:1366-1371(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ishikawa J.;
 RT Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Jang J.S., Kim B.E.;
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Nlickerson D.A.;
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 23-46.
 RX MEDLINE-89246368; PubMed-2655583;
 RA Golds E.E., Mason P., Nyirkos P.;
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
 RT human synovial cells and fibroblasts.";
 RL Biochem. J. 259:585-588(1989).
 RN [9]
 RP SEQUENCE OF 23-54.
 RX MEDLINE-89279141; PubMed-2659722;
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,
 RA Mizuno S.;
 RT "Purification and partial primary sequence of a chemotactic protein
 RT for polymorphonuclear leukocytes derived from human lung giant cell
 RT carcinoma L655C cells.";
 RL J. Exp. Med. 169:1895-1901(1989).
 RN [10]

RP SEQUENCE OF 28-99.
 RX MEDLINE-88162914; PubMed-3279957;
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;
 RT "Structure determination of a human lymphocyte derived neutrophil
 RT activating peptide (LYNAP).";
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).
 RN [11]
 RP SEQUENCE OF 28-59.
 RX MEDLINE-88106502; PubMed-3322281;
 RA Walz A., Feveri P., Aschauer H., Baggiolini M.;
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-
 RT activating factor produced by monocytes.";
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).
 RN [12]
 RP SEQUENCE OF 28-69.
 RX MEDLINE-88097462; PubMed-3480540;
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,
 RA Oppenheim J.J., Leonard E.J.;
 RT "Purification of a human monocyte-derived neutrophil chemotactic
 RT factor that has peptide sequence similarity to other host defense
 RT cytokines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).
 RN [13]
 RP N-TERMINAL FORMS.
 RX MEDLINE-91006326; PubMed-2145175;
 RA van Damme J., Rampart M., Conling R., Decock B., van Osselaer N.,
 RA Willems J., Billiau A.;
 RT "The neutrophil-activating proteins interleukin 8 and beta-
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally
 RT processed forms.";
 RL Eur. J. Immunol. 20:2113-2118(1990).
 RN [14]
 RP N-TERMINAL FORMS.
 RX MEDLINE-89231715; PubMed-2523801;
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;
 RT "Purification of granulocyte chemotactic peptide/interleukin-8
 RT reveals N-terminal sequence heterogeneity similar to that of
 RT beta-thromboglobulin.";
 RL Eur. J. Biochem. 181:337-344(1989).
 RN [15]
 RP SYNTHESIS OF 28-99.
 RX MEDLINE-9115767; PubMed-2007144;
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,
 RA Aebbersold R.;
 RT "Chemical synthesis, purification, and characterization of two
 RT inflammatory proteins, neutrophil activating peptide 1
 RT (interleukin-8) and neutrophil activating peptide.";
 RL Biochemistry 30:3128-3135(1991).
 RN [16]
 RP REVIEW.
 RX MEDLINE-92347562; PubMed-1639201;
 RA Baggiolini M., Clark-Lewis I.;
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";
 RL FEBS Lett. 307:97-101(1992).
 RN [17]
 RP STRUCTURE BY NMR.
 RX MEDLINE-90234679; PubMed-2184886;
 RA Clow G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;
 RT "Three-dimensional structure of Interleukin 8 in solution.";
 RL Biochemistry 29:1689-1696(1990).
 RN [18]
 RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.
 RX MEDLINE-99148123; PubMed-10368283;
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;
 RT "Structure of a CXCL chemokine-receptor fragment in complex with
 RT interleukin-8.";
 RL Structure 7:157-168(1999).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE-90216714; PubMed-2182630;
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,
 RA Wlodawer A., Weber I.T.;
 RT "Crystallization of human interleukin-8. A protein chemotactic for

```

RT neutrophils and T-lymphocytes."
RL J. Biol. Chem. 265:6851-6853(1990).
RN [20]
RP X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RA MEDLINE=91171286; PubMed=2005614;
RX Clore G.M., Gronenborn A.M.;
RT "Comparison of the solution nuclear magnetic resonance and crystal
RT structures of interleukin-8. Possible implications for the mechanism
RT of receptor binding."
RL J. Mol. Biol. 217:611-620(1991).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RX MEDLINE=91110556; PubMed=1988949;
RA Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA Yamada M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT "Crystal structure of interleukin 8: symbiosis of NMR and
RT crystallography."
RL Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RX MEDLINE=20178334; PubMed=10707023;
RA Gerber N., Lowman H., Artis D.R., Eigenbrodt C.;
RT "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT structure of the USC/H33C variant at 2.35 A resolution."
RL Protein 38:361-367(2000).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y00787; CAA68742.1; -
DR EMBL: M17017; AAA35611.1; -
DR EMBL: M26383; AAA36323.1; -
DR EMBL: M28130; AAA59158.1; -
DR EMBL: D14283; BAA03245.1; -
DR EMBL: AF043337; AAK00048.1; -
DR EMBL: AF385626; AAK60276.1; ALT_SEQ.
DR PIR: A37034; A37034.
DR PIR: S03975; S03975.

Query Match 26.7%; Score 96.5; DB 1; Length 99;
Best Local Similarity 31.1%; Pred. No. 4.6e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCP-REFESHVARANKHLKILNT-PNCA-LQIVARLKNRRVOCID 52
DB 21 EGAVLPRSAKELRCQCIKTYSKPFHKKFIKELNVIESGPCANTETIIVKL-SDGRCLCD 79
QY 53 PKLKWIOEYIEKAL 66
DB 80 PKENWQVRYVEKFL 93

RESULT 8
ID IL8_MACMU STANDARD; PRT; 101 AA.
AC P51495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.

```

```

OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Bar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=762861;
RA Minnerly J.C., Baganoif M.P., Deppeler C.L., Keller B.T.,
RA Rapp S.R., Wlodecki D.L., Fretland D.J., Bolanowski M.A.;
RT "Identification and characterization of rhesus macaque
RT interleukin-8."
RL Inflammation 19:313-331(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19849; AAA86711.1; -
DR EMBL: U19851; AAA86713.1; -
DR EMBL: S78555; AAA80141.2; -
DR HSSP: P10145; 21L8.
DR InterPro: IPR001089; CXK_cmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXK.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11320 MW; 42BCF9C97C84B5F9 CRC64;

Query Match 25.8%; Score 93.5; DB 1; Length 101;
Best Local Similarity 30.6%; Pred. No. 0.00011;
Matches 22; Conservative 19; Mismatches 22; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCP-REFESHVARANKHLKILNT-PNCA-LQIVARLKNRRVOCID 52
DB 21 EGAVLPRSAKELRCQCIKTYSKPFHKKFIKELNVIESGPCANTETIIVKL-SDGRCLCD 79
QY 53 PKLKWIOEYIEKAL 64
DB 80 PKENWQVRYVEKFL 91

RESULT 9
ID IL8_SHEEP STANDARD; PRT; 101 AA.
AC P36925;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.

```



```

DE      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Interleukin-8 precursor (IL-8) (CXCL8).
CN      IL8.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      11
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95121931; PubMed=7821808;
RX      Legaszelits I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RA      Seow H.F., Yoshimura T., Wood P.R., Colditz I.G.;
RT      "Cloning, sequencing, expression and inflammatory activity in skin of
RT      ovine interleukin-8."
RL      Immunol. Cell Biol. 72:398-405(1994).
CC      -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC      BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC      NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC      RESPONSE TO AN INFLAMMATORY STIMULUS.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC      C-X-C) (CHEMOKINE CXC).
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/).
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X78306; CAA55115.1; -
DR      EMBL: S74436; AAB33241.1; -
DR      PIR: S42496; S42496.
DR      HSSP: P10145; 1IKM.
DR      InterPro: IPR001089; CXC_Chemkine_sm11.
DR      InterPro: IPR001811; Chemokine_IL8.
DR      Pfam: PF00048; IL8; 1.
DR      PRINTS: PRO0437; SMALLCYTCXC.
DR      SMART: SM00199; SCY; 1.
DR      PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR      CYCline: Chemocaxis; Inflammatory response; signal.
FT      SIGNAL 1 22 BY SIMILARITY.
FT      CHAIN 23 101 INTERLEUKIN-8.
FT      DISULFID 34 61 BY SIMILARITY.
FT      DISULFID 36 77 BY SIMILARITY.
SO      SEQUENCE 101 AA; 11292 MW; 40E8418B57C56A5B CRC64;

Query March 25.4%; Score 92; DB 1; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00017;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

OY 3 VSLPQPCRFESHVAVAN--VKHLKILNT-PNCA-LQIVARLKNRRGVCDPKLKW 57
DB 28 MSTELRQC--IKTHSTFHPKFIKELNVIESGPCENSEILVKL-TNGKEVCIDPRKEM 84
OY 58 IOEYLKAL 66
DB 85 VQKVQAFL 93

RESULT 10
SY02_CAVPO STANDARD; PRT; 120 AA.
ID SY02_CAVPO

```

AC		Q08782:	(Rel. 32, Created)
DT	01-NOV-1995	(Rel. 32, Last sequence update)	
DT	01-NOV-1995	(Rel. 32, Last annotation update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1).		
DE	SCTA2 OR MCP1.		
CN	Cavia porcellus (Guinea pig).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.		
OX	NCBL_TaxID=10141.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Z; TISSUE=Spleen;		
RX	MEDLINE=93267104; PubMed=8496603;		
RA	Yoshimura Y;		
RT	"cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of the recombinant protein."		
RL	J. Immunol. 150:5023-5032(1993).		
CC	-I- FUNCTION: CHEMOSTATIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT NEUTROPHILS.		
CC	-I- SUBUNIT: MONOMER OR HOMODIMER. IN EQUILIBRIUM (BY SIMILARITY).		
CC	-I- SUBCELLULAR LOCATION: Secreted.		
CC	-I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMKINE CC).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/cc-or-send-an-email-to-license@isb-sib.ch).		
DR	EMBL: L04985; AAA37047.1; .		
DR	HSSP; P80098; IBCO.		
DR	InterPro: IPRO00827; CC_chemkine_sm1.		
DR	InterPro: IPRO01811; Chemokine_IL8.		
DR	Pfam: PF00048; IL8; 1.		
DR	SMART: SMO0199; SCY; 1.		
DR	PROSITE: PS00472; SMALL_CYTOKINES_CC; 1		
KW	Cytokine; Chemocaxis; Signal; Inflammatory response; Glycoprotein.		
FT	SIGNAL	1..23	BY SIMILARITY.
FT	CHAIN	24..120	SMALL INDUCIBLE CYTOKINE A2.
FT	MOD_RES	24..24	PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT	DISULFID	33..57	BY SIMILARITY.
FT	DISULFID	34..73	BY SIMILARITY.
FT	CARBHYD	97..97	N-LINKED (GLCNAG. . .) (POTENTIAL).
SO	SEQUENCE	120 AA; 13741 MM; 5905596851CF1CS4 CRC64;	
<hr/>			
Query Match 25.4% Score 92; DB 1; Length 120;			
Matches Local Similarity 31.7%; Pred. No. 0.0002;			
Matches 20; Conservative 11; Mismatches 30; Indels 2; Gaps 2;			
DQ	2 GSFLPYRCPCEFFESHVARANKHLKINTPNCAQLAIYARKLNRRNCVIDPKLMIOEY 61 : : : : : : : : : : : : : : : : 27 GVNPTR-TC-CYTEFNQDLKRKYGERITRSSCGEANVIERTLRKKKEVCADPTQMWDY 84		
DY	62 LEK 64 :		
Db	85 IAK 87		
<hr/>			
RESULT 11			
ID	GRO_MOUSE STANDARD; PRG; 96 AA.		
AC	P12850;		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-OCT-1989 (Rel. 12, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Growth regulated protein precursor (CXCL1) (Platelet-derived growth factor-inducible protein KC) (Secretory protein NS1).		

GN SCYB1 OR GRO1 OR GRO OR MGSA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89139485; PubMed=2917992;
 RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
 RT "The platelet-derived growth factor-inducible KC gene encodes a
 RT secretory protein related to platelet alpha-granule proteins.";
 RL J. Biol. Chem. 264:4133-4137(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89078502; PubMed=2909392;
 RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
 RT "Cloning and sequence of a secretory protein induced by growth
 RT factors in mouse fibroblasts.";
 RL Exp. Cell Res. 180:266-275(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,
 RA Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;
 RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96016008; PubMed=7561058;
 RA Ohmori Y., Fukumoto S., Hamilton T.A.;
 RT "Two structurally distinct kappa B sequence motifs cooperatively
 RT control LPS-induced KC gene transcription in mouse macrophages.";
 RL J. Immunol. 155:3593-3600(1995).
 CC -1- FUNCTION: HAS CHEMOKINE ACTIVITY FOR NEUTROPHILS CONTRIBUTES TO
 CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
 CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR, IN LUNG, BY
 CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXK).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: J04596; AAA40131.1; -
 DR EMBL: U20634; AAB03376.1; -
 DR EMBL: U20527; AAB03376.1; JOINED.
 DR EMBL: S79767; -; NOT_ANNOTATED_CDS.
 DR PIR: A32954; A32954.
 DR PIR: JH0081; JH0081.
 DR HSSP: P19875; IONK.
 DR MGD: MGI:108068; Gro1.
 DR InterPro: IPR001089; CXK_chkine.sm11.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCX.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 24 PROBABLE
 FT CHAIN 25 96 GROWTH REGULATED PROTEIN.
 FT DISULFID 33 59 BY SIMILARITY.
 FT DISULFID 35 75 BY SIMILARITY.
 SQ SEQUENCE 96 AA: 10254 MW: 4A52B5E5C3B845C2 CRC64;

Query Match 25.3%; Score 91.5; DB 1; Length 96;
 Best Local Similarity 32.8%; Pred. No. 0.00018;
 Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

OY 8 RCPREFESHVARNYKHLKIL-NTPNCA-LQIVARKNNROVCIIDPKIKIQEYLEKA 65
 DB 32 RCQCLQTMAGIHILKNIQSLKVLSPGPHCTQTEVIATLK-NGRACIDPEAPLVQKIVQKM 90
 OY 66 L 66
 DB 91 L 91
 RESULT 12
 SY05_MOUSE
 ID SY05_MOUSE STANDARD; PRT; 91 AA.
 AC P30882;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A5 precursor (CC15) (T-cell specific RANTES
 DE protein) (SIS-delta) (Murantes).
 GN SCYB5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92277990; PubMed=1375672;
 RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
 RA Krensky A.M., Neilson E.G.;
 RT "Isolation and characterization of cDNA from renal tubular epithelium
 RT encoding murine Rantes.";
 RL Kidney Int. 41:220-225(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92289805; PubMed=1376260;
 RA Schall T.J., Simpson N.J., Mak J.Y.;
 RT "Molecular cloning and expression of the murine RANTES cytokine:
 RT structural and functional conservation between mouse and man.";
 RL Eur. J. Immunol. 22:1477-1481(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss;
 RX MEDLINE=94132613; PubMed=7507961;
 RA Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
 RT "Cloning, genomic organization, and chromosomal localization of the
 RT Scy5 gene encoding the murine chemokine RANTES.";
 RL J. Immunol. 152:1182-1189(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=94217689; PubMed=7513046;
 RA Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,
 RA Paznekas W.A.;
 RT "Definition of a lipopolysaccharide-responsive element in the 5'-
 RT flanking regions of Murantes and crg-2.";
 RL Mol. Cell. Biol. 14:2914-2925(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ, B10.S/J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
 RA R. Z., Teuscher C.;
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
 CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
 CC BASOPHILS AND ACTIVATES EOSINOPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

```

CC  entitles requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch)
-----
DR  EMBL: M77747: AAA40029.1;
DR  EMBL: S37648: AAB22330.1;
DR  EMBL: U02298: AAB18302.1;
DR  EMBL: X70675: CAA50011.1;
DR  EMBL: AF065944: AAC17511.1;
DR  EMBL: AF065945: AAC17512.1;
DR  EMBL: AF065946: AAC17513.1;
DR  EMBL: AF065947: AAC17514.1;
DR  HSSP: P13501: IRTN.
DR  MCD: MGI:98262: SCYA5.
DR  InterPro: IPR000827: CC_chemkine_sml.
DR  InterPro: IPR001811: Chemokine_IL8.
DR  Pfam: PF00048: IL8; 1.
DR  SMART: SM00199: SCY; 1.
DR  PROSITE: PS00472: SMALL_CYTOKINES_CC; 1.
KW  Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT  SIGNAL 1 23 POTENTIAL.
FT  CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
FT  DISULFID 33 57 BY SIMILARITY.
FT  DISULFID 34 73 BY SIMILARITY.
FT  CONFLICT 19 19 T -> A (IN REF. 2).
FT  CONFLICT 41 41 A -> E (IN REF. 1).
SQ  SEQUENCE 91 AA: 10071 MW: 5DFD66F4684FE1C8 CRC64:

Query Match 25.1%; Score 91; DB 1; Length 91;
Best Local Similarity 37.1%; Pred. No. 0.0002;
Matches 23; Conservative 9; Mismatches 24; Indels 6; Gaps 3;

OY 6 PY---RCPCREFSHVA--RANVKHLKILTPNCALQIVARLKNNNROVCDIPKIKWIOE 60
DB 25 PYGSDTTPCCFAYLSLALPRAHKEY-FTYSSKCSMLAVFYTRRNOVCANPEKKWOE 83
OY 61 YL 62
DB 84 YL 85

RESULT 13
SY05_RAT STANDARD: PRT; 92 AA.
ID SY05_RAT
AC P50231:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
DE protein) (SIS-delta).
GN SCYA5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RA Jones M.L., Shanley T.P., Ward P.A.;
RL Submitted (FEB-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CHEMOTACTIC FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC  EMBL: U06436: AAA96499.1;
DR  HSSP: P13501: IRTN.
DR  InterPro: IPR000827: CC_chemkine_sml.
DR  InterPro: IPR001811: Chemokine_IL8.
DR  Pfam: PF00048: IL8; 1.
DR  SMART: SM00199: SCY; 1.
DR  PROSITE: PS00472: SMALL_CYTOKINES_CC; 1.
KW  Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT  SIGNAL 1 24 POTENTIAL.
FT  CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A5.
FT  DISULFID 34 58 BY SIMILARITY.
FT  DISULFID 35 74 BY SIMILARITY.
SQ  SEQUENCE 92 AA: 10170 MW: B4BEC2B420BAC6 CRC64:

Query Match 25.1%; Score 91; DB 1; Length 92;
Best Local Similarity 37.1%; Pred. No. 0.0002;
Matches 23; Conservative 9; Mismatches 24; Indels 6; Gaps 3;

OY 6 PY---RCPCREFSHVA--RANVKHLKILTPNCALQIVARLKNNNROVCDIPKIKWIOE 60
DB 26 PYGSDTTPCCFAYLSLALPRAHKEY-FTYSSKCSMLAVFYTRRNOVCANPEKKWOE 84
OY 61 YL 62
DB 85 YL 86

RESULT 14
IL8_PIG STANDARD: PRT; 103 AA.
ID IL8_PIG
AC P26894: P22951:
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage
DE chemotactic factor 1) (AMCF-1).
GN IL8.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103307; PubMed=8276881;
RA Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,
RA Weiss D.J., Murtough M.P.;
RT "Regulation of interleukin-8 expression in porcine alveolar
RT macrophages by bacterial lipopolysaccharide.";
RL J. Biol. Chem. 269:77-85(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Sanjanwala M.;
RL Submitted (JUL-1991) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.
RC TISSUE=Lung;
RX MEDLINE=93041741; PubMed=1420165;
RA Goodman R.B., Foster D.C., Mathews S.L., Osborn S.G., Kuljper J.L.,
RA Forstrom J.W., Martin T.R.;
RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil
RT chemotactic factors I and II: identification of porcine IL-8 and
RT another intercrine-alpha protein.";
RL Biochemistry 31:10483-10490(1992).
RN [4]
RP REVISION TO 23.
RA Goodman R.B.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 26-45.
RC STRAIN=Yorkshire;
RX MEDLINE=91217086; PubMed=1850745;
RA Goodman R.B., Forstrom J.W., Osborn S.G., Chl E.Y., Martin T.R.;

```

```

RT "identification of two neutrophil chemotactic peptides produced by
RT porcine alveolar macrophages."
RL J. Biol. Chem. 266:8455-8463(1991).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.
CC -1- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M86923; AAA16616.1; -
DR EMBL: X61151; CAA43461.1; -
DR EMBL: M99367; AAA92576.1; -
DR PIR: A44253; A44253.
DR PIR: A39819; A39819.
DR HSSP: P10145; 11KM.
DR InterPro: IPR001089; CXK_chmkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXK.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine: Chemotaxis; Inflammatory response; Signal.
KW SIGNAL.
FT CHAIN 1 25
FT DISULFID 26 103
FT DISULFID 34 61
FT DISULFID 36 77
FT CONFLICT 33 34
FT CONFLICT 87 87
FT CONFLICT K -> KK (IN REF. 2).
SQ SEQUENCE 103 AA: 11633 MW: 9FE0E350E1928C64 CRC64;

Query Match
Best Local Similarity 25.1%; Score 91; DB 1; Length 103;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

QY 3 VSLPRPCPFESHVARAN---VKHLKIILNT-PNCA-LOIVARLKNNNQVCLDRKLW 57
DB 28 VSAELRCQC--INTHSTPFHPKFKELRVIESGPHCENSEIIVKLV-NGREVCIDPREKW 84
QY 58 IOEYLE 63
DB 85 VQKVVO 90

RESULT 15
IL8 CERTO
ID IL8 CERTO STANDARD: PRT: 101 AA.
AC P46653;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;

```

```

RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19839; AAA86705.1; -
DR HSSP: P10145; 21I8.
DR InterPro: IPR001089; CXK_chmkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXK.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine: Chemotaxis; Inflammatory response; Signal.
KW SIGNAL.
FT CHAIN 1 22
FT DISULFID 23 101
FT DISULFID 34 61
FT DISULFID 36 77
FT DISULFID 77 77
FT DISULFID BY SIMILARITY.
SQ SEQUENCE 101 AA: 11309 MW: DE14CEE4BC0889D7 CRC64;

Query Match
Best Local Similarity 24.7%; Score 89.5; DB 1; Length 101;
Matches 22; Conservative 19; Mismatches 24; Indels 9; Gaps 5;

QY 1 KGVSIP-----YRCP-RFESHVARANYKHLKIILNT-PNCA-LOIVARLKNNNQVCLD 52
DB 21 EGAVLPSSAKELRCICIKYTSKPFHPKFKELRVIESGPHCVTEIIVKL-SDGRELCLD 79
QY 53 PKLWIOEYLELAKL 66
DB 80 KPEPWQGVVERKFL 93

```

Search completed: January 23, 2003, 15:34:19
 Job time : 7 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 : Search time 22.6 seconds
(without alignments)
610.848 Million cell updates/sec

Title: US-09-852-424-3
Perfect score: 362
Sequence: 1 KGVSLPYRCPREFSHVAR.....QVCIDPKLKIQVLEKALN 67

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP_virus:*
13: SP-vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	92	4 Q9H554	Q9H554 homo sapien
2	338	93.4	89	11 Q90ZD1	Q90ZD1 ratius norv
3	285	78.7	94	13 Q8U0U9	Q8U0U9 xenopus lae
4	93.5	25.8	91	11 Q91ZL1	Q91ZL1 sigmond hi
5	88	24.3	98	13 Q8QGV8	Q8QGV8 paraliichy
6	88	24.3	109	13 Q8QY59	Q8QY59 paraliichy
7	88	24.3	148	11 Q9QYD7	Q9QYD7 mus musculu
8	82.5	22.8	79	4 Q95689	Q95689 homo sapien
9	82.5	22.8	134	12 Q9YV49	Q9YV49 gallid herp
10	82.5	22.8	142	12 Q91BJ7	Q91BJ7 turkey herp
11	82	22.7	104	13 Q73912	Q73912 gallus galli
12	82	22.7	203	12 Q67634	Q67634 marek s dis
13	79.5	22.0	101	13 Q93442	Q93442 lampetra fl
14	79.5	22.0	108	6 Q28724	Q28724 oryctolaugus
15	78	21.5	97	13 Q98TQ2	Q98TQ2 oncorhynchu
16	77.5	21.4	97	6 Q9TTS6	Q9TTS6 bos taurus

17	76.5	21.1	100	11 Q91ZK9	Q91ZK9 sigmond hi
18	76.5	21.1	101	11 Q91Z64	Q91Z64 sigmond hi
19	76.5	21.1	363	13 Q90ZT0	Q90ZT0 brachydanio
20	76.5	21.1	1096	13 Q90ZT1	Q90ZT1 brachydanio
21	76	21.0	101	13 Q8UW91	Q8UW91 tritakis scy
22	76	21.0	106	11 Q92292	Q92292 cricetus
23	75.5	20.9	91	13 Q8Q556	Q8Q556 gallus galli
24	75.5	20.9	883	13 Q91493	Q91493 torpedo cal
25	74.5	20.6	97	13 Q8QFP5	Q8QFP5 cyprinus ca
26	73.5	20.3	97	11 Q92318	Q92318 cavia porce
27	73.5	20.3	126	11 Q99J60	Q99J60 mus musculu
28	73.5	20.3	601	13 Q73928	Q73928 scyllorhinu
29	72.5	20.0	95	12 Q98158	Q98158 kaposi's sa
30	70	19.3	91	13 Q8Q557	Q8Q557 gallus galli
31	69.5	19.2	92	6 Q8S040	Q8S040 felis silve
32	69	19.1	80	4 Q1745	Q1745 homo sapien
33	69	19.1	93	4 Q96168	Q96168 homo sapien
34	69	19.1	96	13 Q90825	Q90825 gallus galli
35	69	19.1	395	11 Q91V44	Q91V44 mus musculu
36	68	18.8	89	13 Q918E0	Q918E0 gallus galli
37	68	18.8	102	6 Q95M27	Q95M27 ovis aries
38	67.5	18.6	101	11 Q9EP62	Q9EP62 ratius norv
39	67.5	18.6	116	11 Q91ZB2	Q91ZB2 mus musculu
40	67.5	18.6	1203	5 Q8T1J7	Q8T1J7 dictyostell
41	67.5	18.6	2994	5 Q95ZG5	Q95ZG5 dictyostell
42	67	18.5	62	4 Q95690	Q95690 homo sapien
43	66	18.2	92	11 Q91Z65	Q91Z65 sigmond hi
44	66	18.2	100	6 Q95MD5	Q95MD5 bos taurus
45	65.5	18.1	100	13 Q8QGB7	Q8QGB7 oncorhynchu

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	92 AA.
Q9H554			
AC Q9H554:			
DT 01-MAR-2001 (TRENBLREL. 16, Created)			
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)			
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)			
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)			
DE (Fragment).			
GN SDF1.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBITaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Bird C.;			
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AL137026; CAC10202.1; -			
DR HSSP; P48061; ISDF.			
DR InterPro; IPR001811; Chemokine_IL8.			
DR Pfam; PF00048; IL8; 1.			
DR SMART; SM00199; SCY; 1.			
FT NON_TER			
FT SEQUENCE			
FT 92 AA: 10510 MW: AEF0C402B44ED20 CRC64;			

Query Match	95.6%	Score 346:	DB 4:	Length 92:
Best Local Similarity	97.0%	Pred. No. 1.1e-35:		
Matches 65:	Conservative	0:	Mismatches 2:	Indels 0:
			Gaps 0:	

QY	1 KGVSLPYRCPREFSHVARANKHLKINTPCALQIVARLKNNNRQVCIDPKLKIQWIE 60
DB	22 KPVSLPYRCPREFSHVARANKHLKINTPCALQIVARLKNNNRQVCIDPKLKIQWIE 81
QY	61 YLEKALN 67
DB	82 YLEKALN 88

```

RESULT 2
O9QZD1
ID O9QZD1 PRELIMINARY: PRT: 89 AA.
AC O9QZD1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Ohnishi Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
RT alpha).";
RL submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillarsetti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
RT alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF189724; AAF01066.1; -
DR EMBL; AF209976; AAC43506.1; -.
DR HSSP; P48061; ISDF.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA: 9977 MW; D8697526A2E35FA CRC64;

```

Query Match	93.4%	Score 338;	DB 11;	Length 89;
Best Local Similarity	94.0%;	Pred. No. 1.le-34;		
Matches 63;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;
QY 1	KGVSIPYKPCPEFFSFSHARANKVRLKLTINTPNCALQIYARLKNNNQVCIDPKLKWIOE 60			
Db 22	KPVSLSTYKPCPEFFSFSHARANKVRLKLTINTPNCALQIYARLKNNNQVCIDPKLKWIOE 81			
QY 61	YLEKALN 67			
Db 82	YLDKALN 88			
RESULT 3				
Q80U09				
Q80U09	PRELIMINARY;	PRT;	94 AA.	
AC Q80U09:				
DT 01-MAR-2002 (TREMBLrel. 20, Created)				
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE Stromal-derived factor 1 precursor.				
GN SDF-1.				
OS Xenopus laevis (African clawed frog).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;				
OC Xenopodinae; Xenopus.				
OX NCBI_TaxID=8355;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE=SPLEEN;				
RA Brian M., Wunderlin M., Knoechel W., Gierschik P., Moepps B.;				
RT "Xenopus laevis stromal-derived factor 1: conservation of structure				
and function during vertebrate development.";				
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.				
DR EMBL: AJ278857; CACB2196.1; -				
DR InterPro: IPR001811; Chemokine_IL8.				
DR Pfam: PF00048; IL8; 1.				
DR SMART: SM00199; SCY; 1.				
KW Signal.				

FT	SIGNAL	1	21	POTENTIAL	
FT	CHAIN	22	94	STROMAL-DERIVED FACTOR 1	
SO	SEQUENCE	94 AA:	10701 MM:	8C8325D152F32E7	CR664;
	Query Match	78.7%	Score 285;	DB 13;	Length 94;
	Best Local Similarity	74.6%	Pred: 4.7e-28;		
	Matches	50; Conservative	11; Mismatches	26; Indels	0; Gaps 0;

Oy	1	KVSLPYRCGCRFEESHVARAVKHILTLINPCNLOIIVARLKNRNOVCIDPKWIOE	68
Dd	22	KPVSLVYRCRCRRFESNVFKSNIKHILKILTSTNCSLQIVANLKINGOICDPRTXWIOE	81
Oy	61	YLEKALN	67
Dd	82	YLEKALN	88

```

RESULT 4
Q91ZLI
ID Q91ZLI PRELIMINARY; PRT; 91 AA.
AC Q91ZLI;
DT 01-DEC-2001 (TReMBLrel . 19, Created)
DT 01-DEC-2001 (TReMBLrel . 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel . 20, Last annotation update)
DE RAYTES chemokine.
OS Sigmmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pietreva L.M., Prince G.A.;
RT "Sigmmodon hispidus cytokines, chemokines and interferons."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421391; AAL16933.1;
DR InterPro; IPR000827; CC, chemkine, sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
SQ SEQUENCE 91 AA; 10082 MW; DDD6EAEABE42422F CRC64;

```

Query Match	25.8%;	Score 93.5;	DB 11;	Length 91;
Best Local Similarity	38.2%;	Pred. No. 0.00039;		
Matches 21;	Conservative 9;	Mismatches 22;	Indels 3;	Gaps 2;

Qy 10 PCRF--FESHVARANKHLKILNTPNCALQIYARLKNNNROVCIIDPKIKWIOEYL 62
||| : ||| : | : ||||| : ||| : ||| :
Db 32 PCCFAYLSAVLPRAHKEY-FYTSKCSNFAYFVTRNRQVCANPCKKKWQEYI 85

RESULT 5			
ID	Q8QGV8	PRELIMINARY:	PRT; 98 AA.
AC	Q8QGV8;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	CXC chemokine.		
GN	CXC CHEMOKINE.		
OS	Paralichthys olivaceus (Flounder).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;		
OC	Pleuronectoidae; Paralichthyidae; Paralichthys.		
OX	NCBI_TaxID=8235;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Aoki T., Hirono I., Iwachi A.;		
RT	"Molecular cloning and expression of IL-1b and two types of chemokines		
RT	in Japanese flounder, Paralichthys olivaceus.";		
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.		
EMBL	AB070837; BAB86884.1; -		

```

SO SEQUENCE 98 AA: 10846 MW: 495CA4839A5D8C92 CRC64:
Query Match 24.3%; Score 86; DB 13; Length 98;
Best Local Similarity 31.9%; Pred. No. 0.002;
Matches 22; Conservative 17; Mismatches 24; Indels 6; Gaps
OY 2 GVSLEPRPCRFEEFHVAVANVYKHLKILNTP--C-AIQIVARLKNNNQVCIDPLKWI 58
DB 30 GVSLE--HRCRTETESRPIGRVYKSVETI-SPNSHCDKTEIITATLKDGVGLCLDPEAPVW 86
OY 59 QEYLEKALN 67
DB 87 KRIVINKLIS 95

RESULT 6
O90Y59 PRELIMINARY; PRT; 109 AA.
AC O90Y59;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Interleukine-8.
GN IL-8.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpho; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthidae; Paralicthys.
OX NCBI_Taxid=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435923; PubMed=11551708;
RA Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;
RT "Cloning and sequence analysis of the interleukin-8 gene from flounder
RT (Paralicthys olivaceus).";
RL Gene 274;237-243(2001).
DR EMBL; AF216646; AAL05442.1;
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PFO0048; IL8; 1.
SQ SEQUENCE 109 AA: 12117 MW: C7CEI8986C50A6ED CRC64:

Query Match 24.3%; Score 86; DB 13; Length 109;
Best Local Similarity 31.9%; Pred. No. 0.0023;
Matches 22; Conservative 17; Mismatches 24; Indels 6; Gaps
OY 2 GVSLEPRPCRFEEFHVAVANVYKHLKILNTP--C-AIQIVARLKNNNQVCIDPLKWI 58
DB 29 GVSLE--HRCRTETESRPIGRVYKSVETI-SPNSHCDKTEIITATLKDGVGLCLDPEAPVW 85
OY 59 QEYLEKALN 67
DB 86 KRIVINKLIS 94

RESULT 7
O90YD7 PRELIMINARY; PRT; 148 AA.
AC O90YD7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Small inducible cytokine A2.
GN SCYA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SL/J; TISSUE=SPLEEN;
RX MEDLINE=99370037; PubMed=104389970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,

```

RA	Blankenhorn E.P.:
RT	"Sequence polymorphisms in the chemokines Sclay (TCA-3), SCy2
RT	(monocyte chemoattractant protein (MCP)-1), and Sclay2 (MCP-5) are
RT	candidates for eaey, a locus controlling susceptibility to monophasic
RT	remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL	J. Immunol. 163:1266-1266(1999).
DR	EMBL; AF065929; AAF15379.1; "-.
DR	HSSP; P13500; IDOK.
DR	MGD; MG1:98259; SCy2.
DR	InterPro: IPR000827; CC_chemkine_sml.
DR	InterPro: IPR001811; Chemokine_IL8.
DR	Pfam: PF00048; IL8; 1.
DR	SMART: SM00199; SCY; 1.
DR	PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
SQ	SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489EB CRC64;
OY	Query Match 24.3%; Score 88; DB 11; Length 148;
Db	Best Local Similarity 26.2%; Pred. NO. 0.0031;
	Matches 16; Conservative 14; Mismatches 31; Indels 0; Gaps 0;
OY	63 E 63
Db	88 K 88
RESULT 8	
ID	095689 PRELIMINARY; PRT; 79 AA.
AC	095689;
DT	01-MAY-1999 (TREMBLrel. 10; Created)
DT	01-MAY-1999 (TREMBLrel. 10; last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20; last annotation update)
DE	CC-Chemokine (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=FORESKIN;
RA	Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA	Schroeder J.M.;
RT	"Expression of a MCP-4 like novel CC-chemokine in human dermal
RT	fibroblasts: molecular cloning and RT-PCR analysis."
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR	EMBL; Z77650; CAB0111.1; "-.
DR	HSSP; P51671; EBOT.
DR	InterPro: IPR000827; CC_chemkine_sml.
DR	InterPro: IPR001811; Chemokine_IL8.
DR	Pfam: PF00048; IL8; 1.
DR	SMART: SM00199; SCY; 1.
DR	PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
FT	NON TER 1
SO	SEQUENCE 79 AA; 8987 MW; 4FCF42983DA6C352 CRC64;
OY	Query Match 22.8%; Score 82.5; DB 4; Length 79;
Db	Best Local Similarity 28.6%; Pred. NO. 0.008;
	Matches 18; Conservative 16; Mismatches 24; Indels 5; Gaps 3;
OY	61 YLE 63
Db	69 YMK 71
RESULT 9	

```

09YVA9
ID 09YVA9 PRELIMINARY: PRT: 134 AA.
AC 09YVA9:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE VIL8 (CXC chemokine VIL8).
GN MDV003 OR MDV078.
OS Gallid herpesvirus 1,
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Marek's disease herpesvirus (strain MD5) (MDHV), Turkey herpesvirus.
OC Alphaherpesvirinae: Infection laryngotracheitis-like viruses.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
NCBI_TaxID=10386, 10388, 10389;
RN
RP SEQUENCE FROM N.A.
RC SPECIES-Gallid herpesvirus 1: STRAIN-RB1B;
RA Rassaert D., Fraquet L.;
RT Characterisation of the BamHI L fragment of the Marek's disease virus
RT RB1B strain (serotype 1).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain GA) (MDHV);
RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.;
RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain MD5) (MDV);
RA MEDLINE=20392152; PubMed=10933706;
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
RL J. Virol. 74:7980-7988(2000).
RN
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain MD5) (MDV);
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
RL J. Virol. 74:7980-7988(2000).
RN
RP SEQUENCE FROM N.A.
RC SPECIES-Marek's disease herpesvirus (strain MD5) (MDV);
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF331499; AAL58097.1; -
DR EMBL: AF065430; AAC77449.1; -
DR EMBL: AF243438; AAG14290.1; -
DR EMBL: AF243438; AAG14256.1; -
DR HSSP: P10889; IMI2.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemokine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKXC.
DR SMART: SM00199; SCY; 1.
SQ SEQUENCE 134 AA; 14828 MW; C859CDB86BD25190 CRC64;

Query Match 22.8%; Score 82.5; DB 12; Length 134;
Best Local Similarity 27.5%; Pred. No. 0.014;
Matches 22; Conservative 14; Mismatches 17; Indels 27; Gaps 4;

QY 2 GVSUPLYRCPCRFESHVARANKHLILNTP-----NC-ALQIVARLKN 44
ID 1:11 11 1:1:1 1:1:1
DB 22 GISL-----ESLAVDRCKCKVKTNPRTGPIIADVIPRGHCRTEIFALK- 71
OY 45 NNROYCIDPKLWIOEYLEK 64
ID 1:1:1:1:1 1:1:1:1:1
DB 72 KNRKVCVDPAPWVOQFIKK 91

RESULT 10
Q9IBJ7 PRELIMINARY: PRT: 142 AA.
AC 09IBJ7:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE VIL-8.
GN R-LORF2.

```

```

OS Turkey herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae;
OC Alphaherpesvirinae: Marek's disease-like viruses.
NCBI_TaxID=10390;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RX MEDLINE=92237304; PubMed=1315048;
RA Jones D., Lee L., Liu J.L., Kung H.J., Tillotson J.K.;
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
RT the fos/jun oncogenes that is highly expressed in lymphoblastoid
RT tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RA Lee L.F., Wu P., Sui D., Ren D., Kung H.J.;
RT "The Complete UL Sequence of Serotype I Marek's Disease Virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR EMBL: AF147806; AAF67205.1; -
DR EMBL: AF147806; AAF66793.1; -
DR HSSP: P10889; IMI2.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemokine_sm11.
DR InterPro: IPR001230; Prey1_site.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 142 AA; 15770 MW; 35A8CE9B92FD209 CRC64;

Query Match 22.8%; Score 82.5; DB 12; Length 142;
Best Local Similarity 27.5%; Pred. No. 0.014;
Matches 22; Conservative 14; Mismatches 17; Indels 27; Gaps 4;

QY 2 GVSUPLYRCPCRFESHVARANKHLILNTP-----NC-ALQIVARLKN 44
ID 1:11 11 1:1:1 1:1:1
DB 22 GISL-----ESLAVDRCKCKVKTNPRTGPIIADVIPRGHCRTEIFALK- 71
OY 45 NNROYCIDPKLWIOEYLEK 64
ID 1:1:1:1:1 1:1:1:1:1
DB 72 KNRKVCVDPAPWVOQFIKK 91

RESULT 11
Q73912 PRELIMINARY: PRT: 104 AA.
AC 073912:
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE K60 protein precursor (CXC chemokine K60).
GN K60.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN
RP SEQUENCE FROM N.A.
RC TISSUE-MACROPHAGE LIKE;
RA Sick C.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=20170941; PubMed=10704244;
RA Sick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXC and CC chemokines.";
RL Cytokine 12:181-186(2000).
RN
RP SEQUENCE FROM N.A.
RA Hughes S.M., Bumstead N.;
RT "Mapping of a second ELR CXC chemokine to chicken chromosome four.";

```



```

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y14971; CAA75212.1; -.
DR EMBL: AF277660; AAF66485.1; -.
DR HSSP: P02775; ITVX.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemkine_sml1.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT CHAIN 21 104 POTENTIAL.
FT CHAIN 21 104 K60 PROTEIN.
SQ SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;

Query Match
Best Local Similarity 22.7%; Score 82; DB 13; Length 104;
Matches 19; Conservative 20; Mismatches 22; Indels 8; Gaps 4;

OY 4 SUPRCRCFFESHVARANKHLKILNT---PNCALQIVARLKNNNQVCIIDPKLKI 58
DB 29 AILKRCQC--IEHSHKFIHKFIONVNLTPSGHCKNVEVIATLK-DGREVCUDPTAPV 85
OY 59 OEYLEKALN 67
DB 86 KLITKALD 94

RESULT 12
O67634 PRELIMINARY; PRT; 203 AA.
ID 067634;
AC 067634;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Eco Q protein (Fragment).
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN 111;
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RX MEDLINE-96074534; PubMed-7491783;
RA Peng Q., Zeng M., Bhulian Z.A., Ubukata E., Tanaka A., Nonoyama M.,
RA Shitazi Y.;
RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
RT mapping to the BamHI-12, BamHI-Q2, and BamHI-L fragments of the MDV
RT genome from lymphoblastoid cells transformed and persistently infected
RT with MDV."
RL Virology 213:590-599(1995).
DR EMBL: U34966; AAC54629.1; -.
DR HSSP: P10889; IM12.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemkine_sml1.
DR InterPro: IPR004827; TF_bZIP.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKXC.
DR SMART: SM00338; BRLZ; 1.
DR SMART: SM00199; SCY; 1.
FT NON_TER.
FT NON_TER 1 1.
SQ SEQUENCE 203 AA; 23137 MW; DE42F2A1C1A71C88 CRC64;

Query Match
Best Local Similarity 22.7%; Score 82; DB 12; Length 203;
Matches 19; Conservative 17; Mismatches 13; Indels 32; Gaps 4;

OY 1 KGVSLPYRCRCFFESHVARANKHLKILNT-----NCALQIVARLK 43
DB 95 ESIAVVKRCQC-----VKVTRPTGLPIIAVDVIPPCHICRTEIILFALK 140
OY 44 NNRQVCIDPKLKIOWEYLEK 64
||:||||:|:|:||||:|

```

```

DB 141 -KNRKYCVDEAPWQOIFIKK 160

RESULT 13
ID 093442; PRELIMINARY; PRT; 101 AA.
AC 093442;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE LfCA-1 protein precursor.
OS Lampetra fluviatilis (River lamprey).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN 111;
RP SEQUENCE FROM N.A.
RC TISSUE=LEUKOCYTES;
RA Najakshin A.M., Mechetina L.V., Alabyev B.Y., Taranin A.V.;
RT "Identification of the interleukin 8 homologue in lamprey (Lampetra
RT fluviatilis): early evolutionary divergence of chemokines."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ231072; CAA13114.1; -.
DR HSSP: P02775; ITVX.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemkine_sml1.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKXC.
DR SMART: SM00199; SCY; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 23 101.
FT CHAIN 23 101 LfCA-1 PROTEIN.
SQ SEQUENCE 101 AA; 11095 MW; 80CFEE81EA7336D2 CRC64;

Query Match
Best Local Similarity 22.0%; Score 79.5; DB 13; Length 101;
Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;

OY 8 RCRCRCFFESHVARANY--KHLK----LNTPNCA-LQIVARLKNNNQVCIIDPKLKIOWE 60
DB 30 RCQC---VHVISKFIHKFIOETMEVIPPSSNCKNVEIITVMKSTNQICLNDAPVWR 85
OY 61 YLEKALN 67
DB 86 VISHILD 92

RESULT 14
ID 028724; PRELIMINARY; PRT; 108 AA.
AC 028724;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE GRO (Permeability factor 2).
GN RPF2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 111;
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RA Yoshimura T., Modi W.S.;
RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC
RT chemokine subfamily in mammals."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 43-108 FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RX MEDLINE-95129889; PubMed-7828903;
RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA Martin T.R.;

```

RT "Cloning of two rabbit GRO homologues and their expression in alveolar
 RT macrophages."
 RL Gene 151:337-338(1994).
 DR EMBL: U95808; AAB93924.1; -
 DR EMBL: L28933; AAA66975.1; -
 DR HSSP: P19875; 10NK.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL1; Chemokine_sm1.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTFCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match 22.0%; Score 79.5; DB 6; Length 108;
 Best Local Similarity 27.4%; Pred. No. 0.026;
 Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

QY 8 RCPGFFSHVARNVHKLILNT-PPNCA-LQIVARLKNNNROYCIDPKLWIEYLEKA 65
 Db 43 RCOCLQTVGGIHLKSIQSLKVLSPHCAQTEVIATLK-SQGEACLNPAAPMVKFLQKR 101
 QY 66 LN 67
 Db 102 LS 103

RESULT 15

098T02 PRELIMINARY; PRT; 97 AA.

AC 098T02; 01-JUN-2001 (TREMURel. 17, Created)

DT 01-JUN-2001 (TREMURel. 17, Last sequence update)

DT 01-JUN-2002 (TREMURel. 21, Last annotation update)

DE Putative interleukin 8 (Putative cxc chemokine precursor).

GN IL-8.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.*

RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;

RT "Identification and analysis of the interleukin 8 molecule in rainbow

trout Oncorhynchus mykiss.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RA Sangrador-Vegas A., Smith T.J.;

RT "Molecular cloning of a rainbow trout (Oncorhynchus mykiss) CXC

chemokine by use of suppression subtractive hybridization.";

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;

RT "Identification and analysis of the interleukin 8 molecule in rainbow

trout Oncorhynchus mykiss.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ279069; CAC33585.1; -

DR EMBL: AJ300835; CAC45061.1; -

DR EMBL: AJ310565; CAC83945.1; -

DR HSSP: P19875; 10NK.

DR InterPro: IPR001811; Chemokine_IL8.

DR InterPro: IPR001089; CXCL1; Chemokine_sm1.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTFCXC.

DR SMART: SM00199; SCY; 1.

KM SIGNAL.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 97 PUTATIVE CXC CHEMOKINE.

SQ SEQUENCE 97 AA; 10777 MW; 4EBB35A4EF9DACE2 CRC64;

Query Match 21.5%; Score 78; DB 13; Length 97;
 Best Local Similarity 25.0%; Pred. No. 0.036;
 Matches 17; Conservative 18; Mismatches 31; Indels 2; Gaps 2;

QY 1 KGVSLPYRCPGFFSHVARNVHKLIL-NTNCA-LQIVARLKNNNROYCIDPKLWIEYLEKA 58
 Db 26 RGMGADLRRCRCIETESRRIGRLIKRVEMFPSSHCRTEIATLSKSGEICLDVSAAPW 85
 QY 59 OEYLEKAL 66
 Db 86 KRVIEKML 93

Search completed: January 23, 2003, 15:36:20
 Job time : 23.6 secs

PA	(CHEM-)CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
DR	WPI; 2002-106073/14.
XX	
PT	Promoting the rate of haematopoietic cell multiplication for treating a
PT	cancer involves administering chemokine receptor antagonist to the
PT	cells
XX	
PS	Claim 9; Page 54; 68pp; English.
XX	
CC	The invention relates to a method of promoting the rate of haematopoietic
CC	cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC	antagonist (AAm48656-AAm48701) to haematopoietic cells. The antagonist
CC	has cytostatic and immunosuppressive activity and is useful for treating
CC	cancer or autoimmune disease in a patient; to promote the rate of
CC	haematopoietic cell multiplication; to formulate a medicament for
CC	increasing the circulation of the haematopoietic cells in a patient; for
CC	mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC	locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC	CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC	self-renewal, expansion and proliferation of peripheralisation in vivo.
XX	
SO	Sequence 67 AA:
	Query Match 100.0%; Score 359; DB 23; Length 67;
	Best Local Similarity 100.0%; Pred. No. 1.7e-39;
	Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 KGVSLSPRCPCRFESHVARANVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIQE 60
DB	1 KGVSLSPPRCPCRFESHVARANVKHLKILTPNCALQIVARLKNNNROYCIDPKLKWIQE 60
OY	61 YLEKALN 67
DB	61 YLEKALN 67
RESULT 2	
ID	AAm48656
	AAm48656 standard; peptide; 67 AA.
AC	AAm48656;
XX	
DT	20-MAY-2002 (first entry)
XX	
DE	CXCR4 peptide antagonist SEQ ID NO 1.
XX	
KW	CRCX4; haematopoietic cell; chemokine receptor-4; cytoslastic;
KW	immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
XX	cell multiplication.
OS	Synthetic.
XX	
PN	WO200185196-A2.
XX	
PD	15-NOV-2001.
XX	
PF	09-MAY-2001; 2001WO-CA00659.
XX	
PR	09-MAY-2000; 2000CA-2305787.
XX	
PR	19-MAY-2000; 2000US-205467B.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
WR	WPI; 2002-106073/14.

Pt		Promoting the rate of haematopoietic cell multiplication for treating a
Pt		cancer involves administering chemokine receptor antagonist to the
Pt		cells -
xx		
PS		Claim 9; Page 54; 68pp; English.
xx		
CC		The invention relates to a method of promoting the rate of haematopoietic
CC		cell multiplication comprising administering chemokine receptor-4 (CXCR4),
CC		antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC		has cytostatic and immunosuppressive activity and is useful for treating
CC		cancer or autoimmune disease in a patient; to promote the rate of
CC		haematopoietic cell multiplication; to formulate a medicament for
CC		increasing the circulation of the haematopoietic cells in a patient; for
CC		mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC		locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC		CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC		self-renewal, expansion and proliferation of peripheralisation in vivo.
xx		
SQ		Sequence 67 AA:
	Query Match	97.2%; Score 349; DB 23; Length 67;
	Best Local Similarity	98.5%; Pred. No. 3.5e-38;
	Matches 66; Conservative	0; Mismatches 1; Indels 0; Gaps 0.
OY	1 KGVSLSPPRCPEFFESHVARANKHLITNPNCALQIYARLKNNNROYCIPDKLKWIOE 60	
Db	1 KGVSLSPRCPEFFESHVARANKHKLITNPNCALQIYARLKNNNROYCIPDKLKWIOE 60	
OY	61 YLEKALN 67	
Db	61 YLEKALN 67	
RESULT 3		
AAM48658		
ID	AAM48658 standard; peptide: 67 AA.	
xx		
AC	AAM48658;	
xx		
DT	20-MAY-2002 (first entry)	
xx		
DE	CXCR4 peptide antagonist SEQ ID NO 3.	
KW	CRGX4; haematopoietic cell; chemokine receptor-4; cytostatic;	
KW	immunosuppressive; cancer; autoimmune disease; peripheral blood locus;	
xx	cell multiplication.	
OS	Synthetic.	
xx		
FH	Key	Location/Qualifiers
FT	Modified-site	6
FT	/note=	"Optionally the proline analogue 6-amino-7-oxo-2,
FT		3,4,5,6,7-hexahydro-1H-indoline-1-carboxylic
FT		acid residue or a bicyclic turned dipeptide
FT		(Bcd)"
xx		
PN	WO200185196-A2.	
xx		
PD	15-NOV-2001.	
xx		
PF	09-MAY-2001; 2001WO-CA00659.	
PR	09-MAY-2000; 2000CA-2305787.	
PR	19-MAY-2000; 2000US-205467P.	
PA	(UYBR-) UNIV BRITISH COLUMBIA.	
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.	
PI	Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;	
PI	Clark-Lewis I, Salari H;	
WI	2002-106073/14.	
DR		
xx		

PT Promoting the rate of haematopoietic cell multiplication for treating a
PT cancer involves administering chemokine receptor antagonist to the
PT cells -
XX
XX
PS Claim 9; Page 54; 68pp; English.
XX
XX The invention relates to a method of promoting the rate of haematopoietic
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC antagonist (AAM48656-AA48701) to haematopoietic cells. The antagonist
CC has cytostatic and immunosuppressive activity and is useful for treating
CC cancer or autoimmune disease in a patient; to promote the rate of
CC haematopoietic cell multiplication; to formulate a medicament for
CC increasing the circulation of the haematopoietic cells in a patient; for
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC self-renewal, expansion and proliferation of peripheralisation in vivo.
XX
SQ Sequence 67 AA:

Query Match 95.8%; Score 344; DB 23; Length 67;
Best Local Similarity 97.0%; Pred. No. 1.6e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
DB 1 KGVSLSPRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
61 YLEKALN 67
61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 4
AAM48657
ID AAM48657 standard; peptide: 67 AA.
XX
AC AAM48657;
XX
DT 20-MAY-2002 (first entry)
XX
DE CXCR4 peptide antagonist SEQ ID NO 2.
XX
KW CRCK4: haematopoietic cell; chemokine receptor-4; cytostatic;
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW cell multiplication.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5 /note= "Optionally the proline analogue 6-amino-7-oxo-2,
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
FT acid residue or a bicyclic turned dipeptide
FT (Brd)"
XX
XX WO200185196-A2.
XX
XX 15-NOV-2001.
XX
XX 09-MAY-2001; 2001WO-CA00659.
XX
XX 09-MAY-2000; 2000CA-2305787.
XX
XX 19-MAY-2000; 2000US-205467P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX Tuden CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI Clark-Lewis I, Salari H;
XX WPI; 2002-106073/14.
XX
XX

PT Promoting the rate of haematopoietic cell multiplication for treating a
PT cancer involves administering chemokine receptor antagonist to the
PT cells -
XX
XX
PS Claim 9; Page 54; 68pp; English.
XX
XX The invention relates to a method of promoting the rate of haematopoietic
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC antagonist (AAM48656-AA48701) to haematopoietic cells. The antagonist
CC has cytostatic and immunosuppressive activity and is useful for treating
CC cancer or autoimmune disease in a patient; to promote the rate of
CC haematopoietic cell multiplication; to formulate a medicament for
CC increasing the circulation of the haematopoietic cells in a patient; for
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC self-renewal, expansion and proliferation of peripheralisation in vivo.
XX
SQ Sequence 67 AA:

Query Match 95.3%; Score 342; DB 23; Length 67;
Best Local Similarity 97.0%; Pred. No. 2.9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
DB 1 KGVSLSPRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
61 YLEKALN 67
61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 5
AAM48660
ID AAM48660 standard; peptide: 67 AA.
XX
AC AAM48660;
XX
DT 20-MAY-2002 (first entry)
XX
DE CXCR4 peptide antagonist SEQ ID NO 5.
XX
KW CRCK4: haematopoietic cell; chemokine receptor-4; cytostatic;
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW cell multiplication.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "Optionally the proline analogue 6-amino-7-oxo-2,
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
FT acid residue"
XX
XX WO200185196-A2.
XX
XX 15-NOV-2001.
XX
XX 09-MAY-2001; 2001WO-CA00659.
XX
XX 09-MAY-2000; 2000CA-2305787.
XX
XX 19-MAY-2000; 2000US-205467P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX Tuden CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI Clark-Lewis I, Salari H;
XX WPI; 2002-106073/14.
XX
XX Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 PS Claim 9: Page 54; 68pp; English.
 XX
 CC The invention relates to a method of promoting the rate of hematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to hematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC hematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the hematopoietic cells in a patient; for
 CC mobilising hematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of hematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates hematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 CC
 SQ Sequence 67 AA:
 Query Match 95.3%; Score 342; DB 23; Length 67;
 Best Local Similarity 97.0%; Pred. No. 2.9e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 DB 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 6
 AAM50760
 ID AAM50760 standard; peptide; 67 AA.
 XX
 AC AAM50760:
 XX
 DT 27-JUL-1998 (first entry)
 XX
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
 XX
 KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
 XX
 OS Homo sapiens.
 XX
 PN FR2751658-A1.
 XX
 PD 30-JAN-1998.
 XX
 PF 26-JUL-1996; 96FR-0009477.
 XX
 PR 26-JUL-1996; 96FR-0009477.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
 XX
 DR WPI; 1998-123039/12.
 XX
 PT Human stromal cell-derived chemokine, SDF-1 - useful for treating
 PT human immunodeficiency virus infection
 XX
 PS Claim 2: Page 29; 48pp; French.
 XX
 CC The invention relates to peptides which bind to a cellular receptor for
 CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
 CC expressed transmembrane domain receptor), especially where the
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or
 CC prevent HIV infections, optionally together with reverse transcriptase
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
 CC receptor antagonists, immunotherapy agents, agents for treating HIV.

CC associated opportunistic infections and/or other CXC or CC chemokines,
 CC especially RANTES, MIP1- alpha , MIP1- beta or MCP1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.
 CC
 SQ Sequence 67 AA:
 Query Match 95.0%; Score 341; DB 19; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.9e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 DB 1 KPVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRVCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 7
 AAY34092
 ID AAY34092 standard; protein; 67 AA.
 XX
 AC AAY34092:
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Native stromal cell derived factor 1 (SDF-1) alpha protein.
 XX
 KW CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KW angiogenesis; stromal cell derived factor 1; SDF-1.
 XX
 OS Mammalia.
 XX
 PN WO9947158-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 12-MAR-1999; 99WO-CA00221.
 XX
 PR 13-MAR-1998; 98CA-2226391.
 PR 14-AUG-1998; 98CA-2245224.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 XX
 PI Clark-Lewis I, Gong J, Duronio V;
 XX
 DR WPI; 1999-561857/47.
 XX
 PT Use of CXC chemokine receptor 4 for treating autoimmune disease and
 PT cancer -
 XX
 PS Example 1: Fig 1; 71pp; English.
 XX
 CC The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)
 CC antagonist for the manufacture of a medicament for reducing interferon
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
 CC to treat or to design a medicament to treat, an autoimmune disease,
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
 CC antagonists may be peptide compounds comprising a substantially purified
 CC peptide fragment, analogue or a pharmacologically acceptable salt of
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents
 CC the amino acid sequence of SDF-1 alpha protein.
 CC
 SQ Sequence 67 AA:
 Query Match 95.0%; Score 341; DB 20; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.9e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 61 YLEKALN 67

RESULT 10
AA67594

ID AAY67594 standard; peptide; 67 AA.

AC AAY67594;

DT 13-JUN-2000 (first entry)

DE SDF-1alpha peptide sequence.

XX SDF-1: CXCR4: CXC chemokine receptor 4; gamma-interferon; cancer; gout;
KM autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KM type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.

XX Unidentified.

PN W0200009152-A1.

PD 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI; 2000-224175/19.

XX Therapeutic composition containing CXCR4 antagonist, useful for
PT treating autoimmune disease, especially multiple sclerosis and cancer
PT

PS Disclosure; Fig 1; 88pp; English.

XX The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells, particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1alpha
CC peptide sequence.
CC

SQ Sequence 67 AA;

Query Match 95.0%; Score 341; DB 21; Length 67;

Best Local Similarity 97.0%; Pred. No. 3.9e-37;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

Db 1 KPVSLSTRCPCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67

Db 61 YLEKALN 67

RESULT 11
AAB47680

ID AAB47680 standard; peptide; 67 AA.

XX AAB47680;

DT 30-JAN-2002 (first entry)

DE SDF-1-alpha.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX Homo sapiens.

PN W0200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001MO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI (CHEM-) CHEMOKINE THERAPEUTICS CORP.

DR WPI; 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
PT

PS Claim 8; Page 57; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
CC

SQ Sequence 67 AA;

Query Match 95.0%; Score 341; DB 23; Length 67;

Best Local Similarity 97.0%; Pred. No. 3.9e-37;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

Db 1 KPVSLSTRCPCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67

Db 61 YLEKALN 67

RESULT 12
AAM50761
ID AAM50761 standard; peptide; 68 AA.
XX AAM50761;

	OS	Homo sapiens.
	XX	Synthetic.
	XX	
	PV	M09920759-A1.
	PD	
	PP	29-APR-1999.
	PF	21-OCT-1998; 98WO-US22282.
	PR	20-OCT-1998; 98US-0175713.
	PR	22-OCT-1997; 97US-0955826.
	PR	27-FEB-1998; 98MO-USO4002.
	PA	(GEMV) GENETICS INST INC.
	PI	
	PT	Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
	DR	Yang O;
	XX	
	DR	WPI: 1999-288307/24.
	N-PSDB:	AAX25530.
	Modified chemokines useful for inhibiting or stimulating angiogenesis	
	Claim 6c: Page 79; 85pp: English.	
	The present sequence represents met-hSDF-1 alpha, i.e. human stromal cell derived growth factor-1 alpha having an added N-terminal methionine residue. DNA encoding met-hSDF-1 alpha (see AAY25530) was produced by cloning an NdeI/XbaI-restricted hSDF-1 alpha PCR product into the E. coli expression vector pAL781 in-frame with an ATG codon. met-hSDF-1 alpha is an example of novel N-terminal modified chemokines (see AAY05818-21) that have at least one Met residue, at least one aminoxy-pentane residue or at least one GroHEK peptide (see AAY05822) covalently attached at the C terminus. The N-terminal modified chemokines are useful for altering receptor function, inhibiting interactions between chemokine receptors and their ligands. They are used as research tools for identifying chemokine receptors, as vaccine adjuvants, as agents for the chemotactic recruitment of migratory cells, as agents for the stimulation or inhibition of angiogenesis, as agents against autoimmune diseases and inflammation, and as agents to inhibit the binding of HIV to certain receptors and the infection of susceptible cells by HIV. HIV infection is best treated with modified SDF-1 alpha and beta or MIP-1 alpha and beta.	
	Sequence 69 AA:	
	Query Match 95.0%; Score 341; DB 20; Length 69; Best Local Similarity 97.0%; Pred.No.4.le-37;	
	Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	1 KGVSLSPGPCPCRFESHVARANVKHLKLINPNCALOIVARLKNNNROYCIDPKLKIOE 60 Db 2 KPVSLSLYPCPCRFESHSVARANVKHLLKLINPNCALOIVARLKNNNROVCIDPKLKIOE 61	
OY	61 YLEKALN 67 Db 62 YLEKALN 68	
RESULT 14		
ID	AAM50762 standard; peptide: 72 AA.	
AC	AAM50762;	
DIT	27-JUL-1998 (first entry)	
DE	Peptide which binds to CXCR4 receptor and is useful for treating HIV.	
FWM	Stromal cell-derived chemokine: SDF-1; human immunodeficiency virus; HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.	

Db 82 YLEKALN 88

RESULT 2
US-08-674-008-1

; Sequence 1, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; APPLICANT: TADA, Hideaki
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; MOLECULE TYPE: protein
; US-08-674-008-1

Query Match 95.0%; Score 341; DB 1; Length 89;
Best Local Similarity 97.0%; Pred. No. 1, 9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPCALQIYARLKNNNROYCIDPKLWIOE 60
Db 22 KPVSLSPRCPCRFESHVARANKHLKILNTPCALQIYARLKNNNROYCIDPKLWIOE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 3
US-08-323-084A-5

; Sequence 5, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: NO. 5563048e1 Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; MOLECULE TYPE: protein
; US-08-323-084A-5

Query Match 95.0%; Score 341; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPCALQIYARLKNNNROYCIDPKLWIOE 60
Db 22 KPVSLSPRCPCRFESHVARANKHLKILNTPCALQIYARLKNNNROYCIDPKLWIOE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 4

US-08-674-008-5
; Sequence 5, Application US/08674008
; Patent No. 5756084

; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; APPLICANT: TADA, Hideaki
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994


```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query Match	94.7%;	Score 340;	DB 1;	Length 89;	
Best Local Similarity	95.5%;	Pred. NO. 2.5e-37;			
Matches 64;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0	
Qy	1	KGVSLSPRCPCFFESHVAVANVHKLTITNFGCALQIAYRLKNNRQVCIDPKLKWIOE	60		
Db	22	KPVSLSTYRCPCFFESHIRAVANVHKLTINTFGCALQIAYRLKNNRQVCIDPKLKWIOE	81		
Qy	61	YLEKALN	67		
Db	82	YLEKALN	88		

RESULT 8
 US-08-330-163-24
 : Sequence 24, Application US/08330163
 : Patent No. 5656724
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Daly, Thomas J.
 : APPLICANT: Larosa, Gregory J.
 : TITLE OF INVENTION: Chemokine-like Proteins and Methods of
 : TITLE OF INVENTION: Use
 :
 : NUMBER OF SEQUENCES: 46
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Fish & Richardson
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 :
 : COUNTRY: U.S.A.
 : ZIP: 02110-2804
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30B

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US//08/330,163
: FILING DATE: 05-AUG-1994
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Fasse, J. Peter
: REGISTRATION NUMBER: 32,983
: REFERENCE/DOCKET NUMBER: 00231/080001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 70 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-330-163-24

```

```

Query Match      26.3%; Score 94.5; DB 1. Length 70;
Best Local Similarity 32.8%; Pred. No. 2.5e-05;
Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3.

QY      8 RCPCHFEASHVARANVKKILNT-PNC-ALQIVARLNNRQVCIDPKLWIOEYLEKA 65
      :| | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      9 QCLCVKTTISQVRPHRITTSLEVYKAGPHCPHTAQLIATLK-NGKKLCLDPRENNVKKIIRKL 67

QY      66 L 66
      |
Db      68 L 68

```

```

1      RESULT 9
2      US-08-482-111-24
3      : Sequence 24, Application US/08482111
4      : Patent No. 5789539
5      : GENERAL INFORMATION:
6      : APPLICANT: Daly, Thomas J.
7      : APPLICANT: Larosa, Gregory J.
8      : TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
9      : TITLE OF INVENTION: Use
10     : NUMBER OF SEQUENCES: 70
11     : CORRESPONDENCE ADDRESS:
12     : ADDRESSEE: Fish & Richardson P.C.
13     : STREET: 225 Franklin Street
14     : CITY: Boston
15     : STATE: MA
16     : COUNTRY: U.S.A.
17     : ZIP: 02110-2804
18     : COMPUTER READABLE FORM:
19     : MEDIUM TYPE: Floppy disk
20     : COMPUTER: IBM PC compatible
21     : OPERATING SYSTEM: PC-DOS/MS-DOS
22     : SOFTWARE: Patentin Release #1.0, Version #1.30B
23     : CURRENT APPLICATION DATA:
24     : APPLICATION NUMBER: US/08/482,111
25     : FILING DATE: 07-JUN-1995
26     : CLASSIFICATION: 514
27     : ATTORNEY/AGENT INFORMATION:
28     : NAME: Fasse, J. Peter
29     : REGISTRATION NUMBER: 32,983
30     : REFERENCE/DOCKET NUMBER: 00231/083001
31     : TELECOMMUNICATION INFORMATION:
32     : TELEPHONE: (617) 542-5070
33     : TELEFAX: (617) 542-8906
34     : INFORMATION FOR SEQ ID NO: 24:
35     : SEQUENCE CHARACTERISTICS:
36     : LENGTH: 70 amino acids
37     : TYPE: amino acid
38     : STRANDEDNESS: single
39     : TOPOLOGY: linear
40     : MOLECULE TYPE: peptide

```


ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-9

Query Match 26.2%; Score 94; DB 1; Length 68;
Best Local Similarity 32.3%; Pred. No. 2.8e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVARANKHLILNT-PNCA-LQIVARLKNNRQVCIDPKLWIOEYLER 64
DB 2 RCQCIKTYSPFHPKFKELRVIESGPHCANTETIVKL-SDGRELCDPKENMVQRYVER 60
QY 65 AL 66
DB 61 FL 62

RESULT 13
US-08-244-702-10
Sequence 10, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578

FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-10

Query Match 26.2%; Score 94; DB 1; Length 68;
Best Local Similarity 32.3%; Pred. No. 2.8e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVARANKHLILNT-PNCA-LQIVARLKNNRQVCIDPKLWIOEYLER 64
DB 2 RCQCIKTYSPFHPKFKELRVIESGPHCANTETIVKL-SDGRELCDPKENMVQRYVER 60
QY 65 AL 66
DB 61 FL 62

RESULT 14
US-08-244-702-11
Sequence 11, Application US/08244702
Patent No. 5665346
GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-244-702-11

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 ; Search time 6.2 Seconds
(without alignments)
218.059 Million cell updates/sec

Title: US-09-852-424-4

Perfect score: 359
Sequence: 1 KGVSLSPRCPCRFESHVAR.....QVCIDPKLKIQETLEKALN 67

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCRT_NEW_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCRTUS_PUBCOMB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	100.0	67	9	US-09-852-424-4
2	350	97.5	67	9	US-09-852-424-8
3	349	97.2	67	9	US-09-852-424-1
4	345	96.1	67	9	US-09-852-424-7
5	344	95.8	67	9	US-09-852-424-3
6	344	95.8	67	9	US-09-852-424-6
7	343	95.5	67	9	US-09-852-424-9
8	342	95.3	67	9	US-09-852-424-2
9	342	95.3	67	9	US-09-852-424-5
10	341	95.0	67	9	US-09-835-107-1
11	341	95.0	67	10	US-09-144-838-8
12	341	95.0	67	10	US-09-144-838-23
13	341	95.0	89	8	US-08-927-939-22
14	341	95.0	89	9	US-09-792-793A-32
15	341	95.0	89	10	US-09-953-682-4
16	341	95.0	89	10	US-09-953-717-4
17	341	95.0	93	8	US-08-927-939-56
18	341	95.0	93	9	US-09-835-107-2
19	341	95.0	93	9	US-09-835-107-3

20	341	95.0	93	9	US-09-792-793A-93	Sequence 93, Appl
21	341	95.0	93	10	US-09-144-838-7	Sequence 7, Appl
22	341	95.0	93	10	US-09-919-497-95	Sequence 95, Appl
23	341	95.0	320	9	US-09-792-793A-77	Sequence 77, Appl
24	341	95.0	322	9	US-09-792-793A-78	Sequence 78, Appl
25	341	95.0	327	9	US-09-792-793A-79	Sequence 79, Appl
26	337.5	94.0	66	9	US-09-852-424-11	Sequence 11, Appl
27	335.5	93.5	66	9	US-09-852-424-12	Sequence 12, Appl
28	330.5	92.1	66	9	US-09-852-424-10	Sequence 10, Appl
29	323.5	90.1	66	10	US-09-144-838-27	Sequence 27, Appl
30	320	89.1	68	10	US-09-144-838-51	Sequence 51, Appl
31	304	84.7	67	10	US-09-144-838-52	Sequence 52, Appl
32	290	80.8	68	10	US-09-144-838-24	Sequence 24, Appl
33	287	79.9	67	10	US-09-144-838-25	Sequence 25, Appl
34	272.5	75.9	67	10	US-09-144-838-28	Sequence 28, Appl
35	269	74.9	69	10	US-09-144-838-52	Sequence 52, Appl
36	266	74.1	68	10	US-09-144-838-53	Sequence 53, Appl
37	253	70.5	68	10	US-09-144-838-48	Sequence 48, Appl
38	250	69.6	67	10	US-09-144-838-49	Sequence 49, Appl
39	249.5	69.5	66	10	US-09-144-838-29	Sequence 29, Appl
40	236	65.7	68	10	US-09-144-838-26	Sequence 26, Appl
41	218.5	60.9	67	10	US-09-144-838-30	Sequence 30, Appl
42	218	60.7	67	10	US-09-144-838-31	Sequence 31, Appl
43	215	59.9	69	10	US-09-144-838-54	Sequence 54, Appl
44	207.5	57.8	66	10	US-09-144-838-35	Sequence 35, Appl
45	199	55.4	68	10	US-09-144-838-50	Sequence 50, Appl

ALIGNMENTS

```

RESULT 1
US-09-852-424-4
; Sequence 4, Application US/09852424
; Patent No. US20020156034A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia; and
APPLICANT: Chemokine Therapeutics Corporation
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: 80021-257
CURRENT APPLICATION NUMBER: US/09/852,424
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: CA 2,305,787
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 60/205,467
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Engineered in
US-09-852-424-4
Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGVSLSPRCPCRFESHVARANKYKHLITPFCALQIVARLKNNNROYCIDPKLKWIOE 60
Db 1 KGVSLSPRCPCRFESHVARANKYKHLITPFCALQIVARLKNNNROYCIDPKLKWIOE 60
QY 61 YLEKALN 67
Db 61 YLEKALN 67
RESULT 2
US-09-852-424-8
; Sequence 8, Application US/09852424

```

```
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (7)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-8
```

```
Query Match          97.5%; Score 350; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 2,1e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
        |||||
```

```
QY      61 YLEKALN 67
        |||||
Db      61 YLEKALN 67
```

```
RESULT 3
US-09-852-424-1
; Sequence 1, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-1
```

```
Query Match          97.2%; Score 349; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 2,7e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
        |||||
```

```
QY      61 YLEKALN 67
        |||||
Db      61 YLEKALN 67
```

```
RESULT 4
US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-7
```

```
Query Match          96.1%; Score 345; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 7,5e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
        |||||
```

```
QY      61 YLEKALN 67
        |||||
Db      61 YLEKALN 67
```

```
RESULT 5
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
```



```
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-5
```

```
Query Match          95.3%; Score 342; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1,6e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNROVCIDPKLKWIOE 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 KGVSLSPRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNROVCIDPKLKWIOE 60
```

```
QY 61 YLEKALN 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 YLEKALN 67
```

```
RESULT 10
US-09-835-107-1
; Sequence 1, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhder
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/222,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SDF-1 alpha
US-09-835-107-1
```

```
Query Match          95.0%; Score 341; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 2.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNROVCIDPKLKWIOE 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 KPVSLSPRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNROVCIDPKLKWIOE 60
```

```
QY 61 YLEKALN 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 YLEKALN 67
```

```
RESULT 11
US-09-144-838-8
; Sequence 8, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
; APPLICANT: Siani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GREN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: US 60/057,620
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8
```

```
Query Match          95.0%; Score 341; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 2.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNROVCIDPKLKWIOE 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 KPVSLSPRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNROVCIDPKLKWIOE 60
```

```
QY 61 YLEKALN 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 YLEKALN 67
```

```
RESULT 12
US-09-144-838-23
; Sequence 23, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
; APPLICANT: Siani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GREN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: US 60/057,620
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-23
```

```
Query Match          95.0%; Score 341; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 2.1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Query Match	95.0%	Score 341;	DB 9;	Length 89;
Best Local Similarity	97.0%;	Pred. No. 2.8e-31;		
Matches 65;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Search completed: January 23, 2003, 15:38:01
Job time : 6.2 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds
(without alignments)
555.259 Million cell updates/sec

Title: US-09-852-424-4

Perfect score: 359

Sequence: 1 KGVSLSPRCPCRFESHVAR.....QVCIDPKLKWIEYLEKALN 67

Scoring table:

BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341	95.0	93	2	G01540
2	340	94.7	89	2	A53497
3	340	94.7	89	2	A53416
4	340	94.7	93	2	I53416
5	101	28.1	101	2	I81182
6	96	26.7	95	2	I48148
7	94	26.2	99	2	JN0841
8	94	26.2	99	2	A37034
9	91.5	25.5	91	1	I48147
10	91.5	25.5	91	1	A46539
11	91	25.3	96	2	A32954
12	90	25.1	103	2	S42496
13	87.5	24.4	103	2	A53096
14	87	24.2	96	2	JN0572
15	86.5	24.1	101	2	I46871
16	86.5	24.0	91	1	A28815
17	83.5	23.3	100	2	A54678
18	82.5	23.0	100	2	JH0200
19	82	22.8	75	2	A54188
20	81.5	22.7	120	2	JE0177
21	81.5	22.7	75	2	B54188
22	81.5	22.7	99	2	I53322
23	80	22.3	119	2	S42881
24	80	22.3	148	1	A30209
25	79.5	22.1	107	2	S07723
26	78.5	21.9	107	2	B38290
27	78.5	21.9	100	2	S21467
28	78.5	21.9	100	2	I55614
29	77.5	21.6	132	2	A57325
			101	2	B28414

ALIGNMENTS

30	77.5	21.6	107	2	A28414	melanoma growth-st
31	77.5	21.6	114	2	A55010	neutrophil-activat
32	77.5	21.6	117	2	B44253	alveolar macrophag
33	76.5	21.3	103	2	A28736	transformation-ind
34	76.5	21.3	103	2	I50417	RSV-induced protei
35	74.5	20.8	96	2	I48099	ectatin precursor
36	74	20.6	92	2	A32393	macrophage inflamm
37	73.5	20.5	107	2	JH0281	macrophage inflamm
38	73.5	20.5	870	2	A41130	dystrophin homolog
39	72.5	20.2	126	2	A35766	platelet factor 4,
40	72	20.1	96	2	JC2478	ectatin precursor
41	71.5	19.9	92	2	I46730	immune activation
42	71.5	19.9	128	1	TGHU	beta-thromboglobul
43	70.5	19.6	53	2	I64831	gene KC protein -
44	69.5	19.4	104	1	PRHUA	platelet factor 4
45	69	19.2	93	2	B35673	LD78-beta protein

RESULT 1

G01540
cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C:Accession: G01540
R:Spocila, L.D.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07697
A:Accession: G01540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <SP>
A:Cross-references: EMBL:016752; NID:q1272194; PID:9571508
C:Superfamily: beta-thromboglobulin

Query Match

Best Local Similarity 95.0%; Score 341; DB 2; Length 93;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KGVSLSPRCPCRFESHVARANKHLINTPCAGLQIVARLKNNNRQVCIDPKLKWIE 60
Db 22 KGVSLSPRCPCRFESHVARANKHLINTPCAGLQIVARLKNNNRQVCIDPKLKWIE 81
Qy 61 YLEKALN 67
Db 82 YLEKALN 88
RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-references: GB:D21072; NID:9413905; PID:BA04648.1; PID:9468457
R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I59582
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>

A:Molecule type: mRNA
A:Residues: 1-99 <RE2>
A:Cross-references: GB:ML7017; NID:g179579; PIDN:AAA35611.1; PID:g179580
R:Kusner, D.J.; Liebberts, E.L.; Nowinski, R.J.; Komieczkowski, M.; King, C.H.; Sedor, J.
Kidney Int. 39, 1240-1248, 1991
A:Title: Cytochrome- and LPS-induced synthesis of interleukin-8 from human mesangial cells
A:Reference number: I37902; MUID:91374977; PMID:1895676
A:Accession: 137902
A>Status: translated from GB/EMBL/DDBU
A:Molecule type: mRNA
A:Residues: 1-97 <RE3>
A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
R:Aloulani, S.; Gaetner, H.F.; Mermod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; P
Eur. J. Biochem. 227, 328-334, 1995
A:Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at t
A:Reference number: S67519; MUID:95154308; PMID:7851404
A:Accession: S67519
A:Molecule type: mRNA
A:Residues: 1-99 <ALO>
C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
C:Comment: This protein is variably processed at the amino end. The major form differs i
C:Genetics:
A:Gene: GDB:IL8
A:Cross-references: GDB:120099; OMIM:146930
A:Map position: 4q13-q421
A:Introns: 22/L: 67/2; 95/2
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-99/Product: interleukin-8, minor form #status experimental <MATA>
F:23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MATF
F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen

Query Match 26.2%; Score 94; DB 2; Length 99;
Best Local Similarity 32.3%; Pred. No. 0.00024;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

OY 8 RCPC-RFEESHAAENVHKLILNT-PNCA-LQIYAFLKNNNRQCIPKIKWIEYLEK 64
|||:::|||||:|:::|:|:|:|:|:|
Db 33 RCQCKITKTSKRPRHFELRLVYESGPHCANTEIVKL-SQRELCDLPKENWGRVVEK 91

OY 65 AL 66
|
Db 92 FL 93

RESULT 8
148147
monocyte chemoattractant protein-1 - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: 148147
R:Toshimura, T.
J. Immunol. 150, 5025-5032, 1993
A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression o
A:Reference number: 148147; MUID:93267104; PMID:8496603
A:Accession: 148147
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: mRNA
A:Residues: 1-120 <RES>
A:Cross-references: GB:I04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C:Genetics:
A:Gene: MCP-1
A:Superfamily: macrophage inflammatory protein

```

Query Match      26.2%  Score 94; DB 2; Length 120;
Best Local Similarity 31.7%  Pred. No. 0.00029;
Matches 20; Conservative 12; Mismatches 29; Indels 2; Gaps 2.

Oy      2  GVSLSPRCCRFEEESHVARANKHILKILTPGCAIQIVARLKNNNNOVQIDPRKWKICEY 61
      ||: :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db      27  GVN-TPPC-CYFNKQIPLKRVKGIERTISSKCPQEAIVLFRLKKNKEVCADPTQKWVDI 84

```

QY	62 LEK 64
	: 1
Db	85 TAK 87

RESULT 9
A46539
monocyte chemoattractant cytokine RANTES precursor - mouse

C.Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
C.Accession: I48875; A46539; I48654; I56370
R.Danoff, T.M.; Lallely, P.A.; Chang, Y.S.; Heeger, P.S.; Nelson, E.G.

A:Title: Cloning, genomic organization, and chromosomal localization of the scya5 gene
A:Reference number: 148875; MUID:94132613; PMID:7507961
A:Accession: 148875
A:Status: preliminary; translated from GR/EMBL/DBJ

ACross-references: EMBL:U02298; NID:g460090; PIDN:AAA18302.1; PID:g460091
Rischall, T.J.; Simpson, N.J.; Mak, J.Y.
Eur. J. Immunol. 22, 1477-1481, 1992

A:Accession: A46539
A:Molecule type: mRNA
A:Residues: 1-18, 'A', '20-91 <SCH>
RTD: 350007
RTD: 350008

A: Note: sequence extracted from NCBI backbone (NCBI:106770, NCBI:106770).
R: Shim, H.S.; Drysdale, B.E.; Shio, M.Y.; Noble, P.W.; Paznekas, W.A.
Mol. Cell. Biol. 14, 2914-2925, 1994

A:Accession: 148654
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Postdoc: 101 <CMT>

A:Title: Isolation and characterization of cDNA from renal tubular epithelium encoding

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-40, 'E', 42-91 <NEI>
Cross-references: GB:M77447; NID:9200649; PTDN:AAA0029.1; PID:9200650

C:Genetics: 26/1; 63/2
A:Introns:
C:Superfamily: macrophage inflammatory protein
C:Keywords: chemotaxis; cytokine; immediate-early protein; inflammation

Query Match	Score 91.5;	DB 1;	Length 91;
Best Local Similarity	37.3%;	Pred. No. 0.00044;	
E:24-91/Product: monocyte	chemoclactacran	cytokine	kanites #status predicted kmh/

```
QY 6 SPRCPREFESHVA--RANVKHLKILNTPNCALQIVARLKNNNRQYCIDPKLWIOEYL 62
    |  | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 28 SDTTPCCFAYLSLALPRAHKEY-FYTSSKCSNIAVVFYTRNRNQYCANPEKKWVOEYI 85
```

```
RESULT 10
A32954
gro-alpha precursor - mouse
```

C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1999
C:Accession: A32934; JH0081

R:Quendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
 J. Biol. Chem. 264, 4133-4137, 1989
 A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protein
 A:Reference number: A32954; MUID:89139485; PMID:2917992
 A:Accession: A32954
 A:Molecule type: mRNA
 A:Residues: 1-96 <COU>
 A:Cross-references: GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043
 R:Ryseck, R.P.; Macdonald-Bravo, H.; Matzel, M.G.; Bravo, R.
 Exp. Cell. Res. 180, 266-275, 1989
 A:Title: Cloning and sequence of a secretory protein induced by growth factors in mouse
 A:Reference number: JH0081; MUID:89078502; PMID:2909392
 A:Accession: JH0081
 A:Molecule type: mRNA
 A:Residues: 1-96 <RVS>
 C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
 C:Genetics: 5
 A:Map position: 5
 C:Superfamily: beta-chromoglobulin
 C:Keywords: extracellular protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-96/Product: gro-alpha #status predicted <MAT>

Query Match 25.5%; Score 91.5; DB 2; Length 96;
 Best Local Similarity 32.8%; Pred. No. 0.00047;
 Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

Oy 8 RCPRFESHVARANVHKIL-LTPNCA-LQIYARLKNRRVOCIDPKLWDEYLEKA 65
 Db 32 RCOCLOTWAGIHLNKLKSLKVLPSGPHCTQTEVIATLK-NGREACLDPEALVOKIVQKM 90
 Oy 66 L 66
 Db 91 L 91

RESULT 11

S42496

Interleukin-8 precursor [similarity] - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-Jan-2001
 C:Accession: S42496; I46997
 R:Legasteleis, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.
 Submitted to the EMBL Data Library, March 1994
 A:Description: Nucleotide sequence of ovine Interleukin 8 cDNA using polymerase chain re
 A:Reference number: S42496
 A:Accession: S42496
 A:Molecule type: mRNA
 A:Residues: 1-101 <LEG>
 A:Cross-references: EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254
 R:Scow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
 Immunol. Cell Biol. 72, 398-405, 1994
 A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte
 A:Reference number: I46997; MUID:95137691; PMID:7835984
 A:Accession: I46997
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-101 <SEO>
 A:Cross-references: GB:S74436; NID:g786590; PIDN:AA833241.1; PID:g786591
 C:Genetics: 8
 A:Gene: IL-8
 C:Superfamily: beta-chromoglobulin
 C:Keywords: chemotaxis; cytokine; inflammation
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-101/Product: Interleukin-8 #status predicted <MAT>

Query Match 25.3%; Score 91; DB 2; Length 101;
 Best Local Similarity 30.4%; Pred. No. 0.00057;
 Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

Oy 3 VSLSPRCRPFESHVARAN--VKHLKILNT-PNCA-LQIYARLKNRRVOCIDPKLKW 57
 Db 28 MSTELRCOC--IKTHSTPFHPKFIKELRVIESGPCENSEIIVKL-TNGKEVCIDPKKEK 84

Oy 58 IOEYLEKAL 66
 Db 85 VQKVVQ 93

RESULT 12

A53096

Interleukin-8 precursor - pig

N:Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Jan-2001
 C:Accession: A53096; A44253
 R:Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta
 J. Biol. Chem. 269, 77-85, 1994
 A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba
 A:Reference number: A53096; MUID:94103307; PMID:8276881
 A:Accession: A53096
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-103 <LIN>
 A:Cross-references: GB:M86923; NID:g164520; PIDN:AAA1616.1; PID:g164521
 R:Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuilper, J.L.; Forstrom,
 Biochemistry 31, 10483-10490, 1992
 A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotac
 A:Reference number: A44253; MUID:93041741; PMID:1420165
 A:Accession: A44253
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-22, 'D', 24-103 <GOO>
 A:Cross-references: GB:M99367; NID:g1235611
 A:Experimental source: alveolar macrophage
 A>Note: sequence extracted from NCBI backbone (NCBI:117415, NCBI:117416)
 A:Note: the sequence in Genbank entry PIGAMCT, release 117.0, has been corrected to
 C:Superfamily: beta-chromoglobulin
 C:Keywords: chemotaxis; cytokine; inflammation
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-103/Product: Interleukin-8 #status predicted <MAT>

Query Match 25.1%; Score 90; DB 2; Length 103;
 Best Local Similarity 31.8%; Pred. No. 0.00077;
 Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

Oy 3 VSLSPRCRPFESHVARAN--VKHLKILNT-PNCA-LQIYARLKNRRVOCIDPKLKW 57
 Db 28 VSAELRCOC--INTHTSPFHPKFIKELRVIESGPCENSEIIVKL-NGKEVCIDPKKEK 84

Oy 58 IOEYLE 63
 Db 85 VQKVVQ 90

RESULT 13

JN0572

Neutrophil chemo-attractant Gro protein precursor - rat

N:Alternate names: CINC; cytokine-induced neutrophil chemoattractant; Interleukin-8-1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
 C:Accession: JN0572; JQ1519; A34481; A48988; B48988; S51214
 R:Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsurufuji, S.; F
 Gene 126, 285-286, 1993
 A:Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
 A:Reference number: JN0572; MUID:93246259; PMID:8482545
 A:Accession: JN0572
 A:Molecule type: DNA
 A:Residues: 1-96 <KON>
 A:Cross-references: DBJ:D11445; NID:g391854; PIDN:BA02009.1; PID:g2020755
 R:Hang, S.; Paulauskis, J.D.; Kobzik, L.
 Biochem. Biophys. Res. Commun. 184, 922-929, 1992
 A:Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
 A:Reference number: JQ1519; MUID:92246987; PMID:1374243
 A:Accession: JQ1519
 A:Molecule type: mRNA

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 : Search time 6 seconds

(without alignments)
463.152 Million cell updates/sec

Title: US-09-852-424-4

Perfect score: 359

Sequence: 1 KGVSLSPRCRCRFESHVAR.....QVCIDPKLKNIQEYLEKALN 67

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	341	95.0	93	SDFL_FELCA	O62657 felis silve
2	341	95.0	93	SDFL_HUMAN	P46061 homo sapien
3	340	94.7	89	SDFL_MOUSE	P40224 mus musculu
4	101	28.1	101	IL8_CAVPO	P49113 cavia porce
5	99	27.6	101	IL8_CANFA	P41324 canis famli
6	96	26.7	101	IL8_FELCA	Q9XSXS felis silve
7	94	26.2	99	IL8_HUMAN	P10145 h interleuk
8	94	26.2	120	SY02_CAVPO	Q08782 cavia porce
9	91.5	25.5	91	SY05_MOUSE	P30882 mus musculu
10	91.5	25.5	92	SY05_RAT	P50231 rattus norv
11	91.5	25.5	96	GRO_MOUSE	P12850 mus musculu
12	91	25.3	101	IL8_MACMU	P51495 macaca mula
13	91	25.3	101	IL8_SHEEP	P36925 ovis aries
14	90	25.1	103	IL8_PIG	P26894 sus scrofa
15	88.5	24.7	91	SY05_CAVPO	P97272 cavia porce
16	88	24.5	101	IL8_BOVIN	P79255 bos taurus
17	88	24.5	130	SY05_RAT	P97885 rattus norv
18	87.5	24.4	96	GRO_RAT	P14095 rattus norv
19	87	24.2	101	IL8_CERTO	P46553 cercocebus
20	87	24.2	101	IL8_RABIT	P18874 oryctolagus
21	86.5	24.1	91	SY05_HUMAN	P13501 homo sapien
22	86	24.0	99	SY07_HUMAN	P80098 homo sapien
23	85.5	23.8	50	SY05_PIG	Q23288 sus scrofa
24	83.5	23.3	100	MIP2_MOUSE	P10889 mus musculu
25	82.5	23.0	114	SY06_HUMAN	P10812 homo sapien
26	81.5	22.7	71	GRO1_RABIT	P30782 oryctolagus
27	81.5	22.7	92	SY03_RAT	P50229 rattus norv
28	81.5	22.7	112	SY06_BOVIN	P80221 bos taurus
29	81.5	22.7	119	SY07_PIG	P43030 sus scrofa
30	81	22.6	120	SY16_HUMAN	O15467 h small ind
31	80	22.3	148	SY02_MOUSE	P10148 mus musculu
32	80	22.3	148	SY02_RAT	P18444 rattus norv
33	79.5	22.1	91	SY05_BOVIN	O97919 bos taurus

34	79.5	22.1	107	1	MI2B_HUMAN	P19876 homo sapien
35	79	22.0	89	1	SY18_HUMAN	P55774 h small ind
36	79	22.0	98	1	SY13_HUMAN	O99616 homo sapien
37	79	22.0	119	1	SY24_MOUSE	O97K00 mus musculu
38	78.5	21.9	100	1	MIP2_RAT	P30348 rattus norv
39	78.5	21.9	132	1	SY05_MOUSE	P50228 mus musculu
40	78	21.7	97	1	SY08_MOUSE	O94121 mus musculu
41	78	21.7	109	1	SY13_HUMAN	O43927 homo sapien
42	77.5	21.6	101	1	GRO_CHICK	P09340 cricetus
43	77.5	21.6	107	1	GRO_HUMAN	P09341 homo sapien
44	77.5	21.6	114	1	SY05_HUMAN	P42830 homo sapien
45	77.5	21.6	117	1	AMC2_PIG	P22952 sus scrofa

ALIGNMENTS

RESULT 1

SDFL_FELCA STANDARD: PRT: 93 AA.

AC O62657: SDFL_FELCA STANDARD: PRT: 93 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
 GN SDF1.

OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;
 RX MEDLINE=98450506; PubMed=9777331;
 RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
 RA Cai J.S., Sato E., Kohmoto M., Mikami T.;

RT "Molecular cloning and sequencing of feline stromal cell-derived
 factor-1 alpha and beta."
 RL Eur. J. Immunogenet. 23:303-305(1998).

CC -! FUNCTION: CHEMOKINE RECEPTOR ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 NOT NEUTROPHILS.
 CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA AND BETA (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -! SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXC).

CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: AB011966; BAA28602.1; -.
 DR HSP: P48061; ISDP.
 DR InterPro: IPR001089; CXC_chmkine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 1 93
 FT SIGNAL 20 93
 FT DISULFID 30 55
 FT DISULFID 32 71
 FT VARSPIC 90 93
 FT SEQUENCE 93 AA; 10581 MW; 44FC763711B9B37 CR664;

Query Match Score 341; DB 1; Length 93;
 Best Local Similarity 97.0%; Pred. No. 6; 1e-35;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	KGVSISPRCPCEFFESHVARANVKKHLINTPNCALQIYARLKNNNROYCIDPKLKWIOE	60
Db	22	KPVSLSYRCPCEFFESHVARANVKKHLINTPNCALQIYARLKNNNROYCIDPKLKWIOE	81
QY	61	YLEKALN	67
Db	82	YLEKALN	88

RESULT 2	SDFL_HUMAN	STANDARD:	PRT:	93 AA.
ID	SDFL_HUMAN			
AC	P48061.			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PSF) (HIRH).			
GN	SDFL			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Spotila L.D.;			
RL	Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96039262; PubMed=7490086;			
RA	Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,			
RA	Shinozawa T., Honjo T.;			
RT	"Structure and chromosomal localization of the human stromal cell-			
RT	derived factor 1 (SDF1) gene.";			
RL	Genomics 28:495-500(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	TISSUE=Liver;			
RA	Begum N.A., Barnard G.F.;			
RT	"Nucleotide sequence of hIRH, human intercrine reduced in			
RT	hepatomas.";			
RL	Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	STRUCTURE BY NMR OF 22-88.			
RX	MEDLINE=98046030; PubMed=9384579;			
RA	Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,			
RA	Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,			
RA	Clark-Lewis I.;			
RT	"Solution structure and basis for functional activity of stromal			
RT	cell-derived factor-1; dissociation of CXCR4 activation from binding			
RT	and inhibition of HIV-1.";			
RL	EMBO J. 16:6996-7007(1997).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.			
RX	MEDLINE=98284037; PubMed=9618518;			
RA	Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,			
RA	Lolis E.;			
RT	"Crystal structure of chemically synthesized [N33A] stromal			
RT	cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'			
RT	coreceptor.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).			
CC	-1- FUNCTION: CHEMOKINE-ATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT			
CC	NOT NEUTROPHILS.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA AND BETA (SHOWN HERE);			
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE			
CC	C-X-C) (CHEMOKINE CXC).			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

```
CC entitles requires a license agreement (See http://www.isb-sib.ch/announcement
or send an email to license@isb-sib.ch).-----
```

```
DR EMBL_ U16752; AAA97434.1; -
DR EMBL_ L36033; AAB39332.1; -
DR EMBL_ L36034; AAB39333.1; -
DR EMBL_ U19495; AAB40516.1; -
DR PDB; 1SDF: 28-JUN-98.
PDB; 2SDF: 17-JUN-98.
PDB; 1A15: 12-AUG-98.
DR Genew; HGNC:10672; SDF1.
MIM; 600835; -.
DR InterPro: IPR001089; CXC_chmkine.sm11.
DR InterPro: IPRO01811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cyclokin; Chemotaxis; Growth factor; Signal; Alternative splicing;
KW 3D-structure.
```

```
FT SIGNAL              1      19          POTENTIAL.
FT CHAIN                20     93          STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID             30     55
FT DISULFID            32     71
FT VARSPIC               90     93       MISSING (IN ISOFORM ALPHA).
SQ SEQUENCE           93 AA: 10666 MW: 505B5A29CBB44EBDCR664;
```

```
Query Match                    95.0%; Score 341; DB 1; Length 93;
Best Local Similarity         97.0%; Pred. No. 6.le-35;
Matches   65; Conservative    0; Mismatches   2; Indels    0; Gaps    0;
```

```
Oy      1 KGVSLSPRCPCRFPFSSHARANVKILKLTLPNCALOIVARKLNRRNVCDPKIKWIOE 60
        | ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      22 KPVSLSYCPQCFEFESHAVARANVKKHLTPNPNCALOIVARKLNRRNOVCIDPKIKWIOE 81
Oy      61 YLEKAALN 67
        |||||
Db      82 YLEKAALN 88
```

```
RESULT 3
SDFL_MOUSE ID SDPL_MOUSE STANDARD; PRG: 89 AA.
AC P40224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPARI) (Thymic lymphoma cell stimulating factor) (TLSE).
```

```
DE DE
GN SDF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CX NCBI_TaxID=10090; [1]
RN MEDLINE FROM N.A. RP MEDLINE=94181581; PubMed=8134392; RA Nagasawa T., Kikutani H., Yoshimoto T.; "Molecular cloning and structure of a pre-B-cell growth-stimulating factor." J. Biol. Acad. Sci. U.S.A. 91:2305-2309(1994). RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994). RN [12]
RP SEQUENCE FROM N.A. RP MEDLINE=93342488; PubMed=8342023; RA Tashiro K., Tada H., Heiker R., Shiozu M., Nakano T., Honjo T.; "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins." Science 261:600-603(1993). RL [13]
RN SEQUENCE FROM N.A. RP MEDLINE=95073497; PubMed=7982471; RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,
```


RA Weinstein I.B. ;
 RT "Molecular cloning of TPARI, a gene whose expression is repressed by
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
 RL Exp. Cell Res. 215:284-293(1994).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AKR/J;
 RA Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G. ;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 NOT NEUTROPHILS.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
 PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
 CC STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D21072; BAA04648.1; -
 DR EMBL: L12029; AAA40100.1; -
 DR EMBL: L12030; AAA40101.1; -
 DR EMBL: S74318; AAB32650.1; -
 DR EMBL: D43804; BAA07862.1; -
 DR EMBL: D43805; BAA07863.1; -
 DR PIR: A53497; A53497.
 DR HSSP: P48061; ISDF.
 DR MGD: MGI:103556; Sdfl.
 DR InterPro: IPR001089; CXCL_chm_kine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 DR Cytokine: Chemotaxis; Growth factor; Signal; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.
 FT DISULFID 30 55
 FT DISULFID 32 71 BY SIMILARITY.
 FT VARSPLIC 89 89 K -> KRLKM (IN ISOFORM BETA).
 SQ SEQUENCE 89 AA: 10032 MW: C48BAD69078E55FA CRC64;
 Query Match 94.7%; Score 340; DB 1; Length 89;
 Best Local Similarity 95.5%; Pred. No. 7.7e-35;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSLSPRCPCRFESHVARANKHLINTPCALQIVARLKNNRNOVCIDPKLWIOE 60
 DB 22 KPVSLSPRCPCRFESHVARANKHLINTPCALQIVARLKNNRNOVCIDPKLWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88
 RESULT 4
 IL8_CANVO STANDARD: PRT; 101 AA.
 ID IL8_CANVO
 AC P49113;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein
 DE 1) (NAP-1).
 GN IL8.
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=94065176; PubMed=7504015;
 RA Yoshimura T., Johnson D.G. ;
 RT "CDNA cloning and expression of guinea pig neutrophil attractant
 protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";
 RL J. Immunol. 151:6225-6236(1993).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L04986; AAA37049.1; -
 DR HSSP: P10145; 2IL8.
 DR InterPro: IPR001089; CXCL_chm_kine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR Cytokine: Chemotaxis; Inflammatory response; signal.
 FT SIGNAL 1 22
 FT CHAIN 23 101 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA: 11414 MW: 557E2A9E15F6727F CRC64;
 Query Match 28.1%; Score 101; DB 1; Length 101;
 Best Local Similarity 35.9%; Pred. No. 1.4e-05;
 Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;
 QY 8 RCPGRFESHVARAN--VKHLKILNT-PMCA-LQIVARLKNNRNOVCIDPKLWIOEYL 62
 DB 33 RCGC--IKIHPTPFHPRFKELKLVIESGPCANSEIIVKL-SNNRQCLDPKKKWQDVV 89
 QY 63 EKAL 66
 DB 90 SMFL 93
 RESULT 5
 IL8_CANFA STANDARD: PRT; 101 AA.
 ID IL8_CANFA
 AC P41324;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010328; PubMed=7916715;
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K. ;
 RT "Cloning of a canine gene homologous to the human

RT Interleukin-8-encoding gene.";
 RL Gene 131:305-306(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-lymph node;
 RX MEDLINE=95127913; PubMed=7827282;
 RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,
 RA Goltzuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshinara K.,
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;
 RT "Molecular cloning and expression of canine Interleukin 8 cDNA.";
 RL Cytokine 6:455-461(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mongrel; TISSUE=Jugular vein;
 RX MEDLINE=95114148; PubMed=7814650;
 RA Kukitaka G.L., Smith W.C., Larosa G.J., Manning A.M.,
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,
 RA Michael L.H., Rot A., Entman M.L.;
 RT "Interleukin-8 gene induction in the myocardium after ischemia and
 RT reperfusion in vivo.";
 RL J. Clin. Invest. 95:89-103(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beagle;
 RX MEDLINE=97230298; PubMed=9119462;
 RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;
 RT "Borrelia burgdorferi migrates into joint capsules and causes an up-
 RT regulation of interleukin-8 in synovial membranes of dogs
 RT experimentally infected with ticks.";
 RL Infect. Immun. 65:1273-1285(1997).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS.
 CC -1- SUBUNIT: HOMODIMER. (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXK).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D28772; BAA05961.1; -;
 DR EMBL: D14285; BAA03246.1; -;
 DR EMBL: U10308; AAC48434.1; -;
 DR EMBL: AF048717; AAC05134.1; -;
 DR HSSP: P10145; 1IKM.
 DR InterPro: IPR001089; CXK_chmkine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTRKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 101 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;

Query Match 27.6%; Score 99; DB 1; Length 101;
 Best Local Similarity 36.1%; Pred. No. 2.5e-05;
 Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;

OY 3 VSISPRCPGFFESHVARANKHLKILNT-----PNCALQIVARLKNKNROVCIDPPLKW 57
 DB 28 VSESLRQC--IKTHSPFPKIKELRYIDSGPHCENSEIYKLVNGN-EVCLDPKRW 84

OY 58 IQE---YLEKA 65
 DB 85 VQKVQIFLAKKA 96

RESULT 6
 ID IL8_FELCA STANDARD; PRT; 101 AA.
 AC O9XSX5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straubinger A.F., Simpson K.W., Straubinger R.K.;
 RT "Feline interleukin-8 mRNA.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXK).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF158598; AAD40323.1; -;
 DR HSSP: P10145; 1IKM.
 DR InterPro: IPR001089; CXK_chmkine_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTRKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 101 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;

Query Match 26.7%; Score 96; DB 1; Length 101;
 Best Local Similarity 33.3%; Pred. No. 5.8e-05;
 Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSISPRCPGFFESHVARAN---VKHLKILNT-PNCALQIVARLKNKNROVCIDPPLKW 57
 DB 28 VSESLRQC--IKTHSPFPKIKELRYIDSGPHCENSEIYKLVN-NGKEVCIDPKRW 84

OY 58 IOEYLE 63
 DB 85 VQKVVE 90

RESULT 7
 ID IL8_HUMAN STANDARD; PRT; 99 AA.
 AC P10145; O9C077; O96RG6;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)


```

RT neutrophils and T-lymphocytes."
RL J. Biol. Chem. 265:6851-6853(1990).
RN [20]
RP X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RX MEDLINE-91171286; PubMed-2005614;
RA Clore G.M., Gronenborn A.M.;
RT "Comparison of the solution nuclear magnetic resonance and crystal
RT structures of interleukin-8. Possible implications for the mechanism
RT of receptor binding."
RL J. Mol. Biol. 217:611-620(1991).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RX MEDLINE-91110556; PubMed-1988949;
RA Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA Yamada M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT "Crystal structure of interleukin 8: symbiosis of NMR and
RT crystallography."
RL Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RX MEDLINE-20178334; PubMed-10707023;
RA Gesser N., Lowman H., Artis D.R., Eigenbrot C.;
RT "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT structure of the L5C/H33C variant at 2.35 A resolution."
RL Proteins 38:361-367(2000).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CX-C).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y00787; CA68742.1; -
DR EMBL: M17017; AAA5611.1; -
DR EMBL: M26383; AAA3633.1; -
DR EMBL: M28130; AAA59158.1; -
DR EMBL: D14283; BAA03245.1; -
DR EMBL: AF043337; AAK00048.1; -
DR EMBL: AF385628; AAK60276.1; ALT_SEQ.
DR PIR: A37034; A37034.
DR PIR: S03975; S03975.

Query Match 26.2%; Score 94; DB 1; Length 99;
Best Local Similarity 32.3%; Pred. No. 9.9e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

OY 8 RCPC-REFESHAVANVAKHLKILNT-PNCA-LQIVARLNKNNRQVCIDPKLKWIOEY 64
DB 33 RCQCIKTSKPRPKIKELRVIESGPHCANTEIIVKL-SDGRELCLDKENNVQAVVER 91
OY 65 AL 66
DB 92 FL 93

RESULT 8
ST02_CAVPO STANDARD: PRT; 120 AA.
AC Q08782;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).

```

```

GN SCVA2 OR MCP1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Z; TISSUE=Spleen;
RX MEDLINE-93267104; PubMed-8496603;
RA Yoshimura T.;
RT "cDNA cloning of guinea pig monocyte chemoattractant protein-1 and
RT expression of the recombinant protein."
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER. IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L04985; AAA37047.1; -
DR HSP; P80098; I800.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 120 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY)
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 120 AA; 13741 MW; 5905596851CFC154 CRC64;

Query Match 26.2%; Score 94; DB 1; Length 120;
Best Local Similarity 31.7%; Pred. No. 0.00012;
Matches 20; Conservative 12; Mismatches 29; Indels 2; Gaps 2;

OY 2 GVLSPRCPCREFESHAVANVAKHLKILNTPNCA-LQIVARLNKNNRQVCIDPKLKWIOEY 61
DB 27 GVN-PTTC-CYFNNKQIPKRYKGYRITSSRCPOAVLFRLLKNKEVCADPRQKVVQY 84
OY 62 LEK 64
DB 85 IAK 87

RESULT 9
ST05_MOUSE STANDARD: PRT; 91 AA.
AC P30882;
DT 01-JUL-1993 (Rel. 26; Created)
DT 01-JUN-1994 (Rel. 29; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) ('T-cell' specific RANTES
DE protein) (SIS-delta) (Murantes).
GN SCVA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

FT	CONFLICT	91 AA:	10071 MW;	A ->E (IN REF. 1)	SDFP66FF4684FEC8 CRC64:
SO	SEQUENCE				
QY	Query Match		25.5%;	Score 91.5;	DB 1;
	Best Local Similarity		37.3%;	Pred. No. 0.00018;	
Matches	22;	Conservative	9;	Mismatches	25;
				Indels	3;
				Gaps	2;
Db					
QY	6 SPPRCRPFESHVA--RANKVHLKILNTPNCALDQIVARLKNRRNOVCIDPLKWTIOEVL	62			
	1 1 1 1 : 1 1 1 1 : 1 1 : 1 1 1 1 : 1 1 1 1 : 1 1 1 1 :				
28 SDTTPCCFAYLIALPLRAHVKEY-FYTSSKCSNLAVVFVTBRNRNOVCANPEKKWQEYI	85				
RESULT 10					
ID	SY05_RAT	STANDARD;	PRT;	92 AA.	
AC	P50231:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Small inducible cytokine A5 precursor (CC15) (T-cell specific RANTES protein) (Sis-delta).				
DE	SCYA5.				
GN	Rattus norvegicus (Rat).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Long Evans; TISSUE=Lung;				
RA	Jones M.L., Shanley T.P., Ward P.A.;				
RL	Submitted (FEB-1994) to the EMBL/GenBank/DDB databases.				
CC	-1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES. MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: U06436; AAA96499.1; .				
DR	HSSP: P13501; IRTN.				
DR	InterPro: IPR000827; CC_chemkine_sml.				
DR	InterPro: IPR001811; Chemokine_IL8.				
DR	Pfam: PF00048; IL8; 1.				
DR	SMART: SM00199; SCY; 1.				
DR	PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.				
KW	Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.				
FT	SIGNAL	1	24	POTENTIAL.	
FT	CHAIN	25	92	SMALL INDUCIBLE CYTOKINE A5.	
FT	DISULEPID	34	58	BY SIMILARITY.	
FT	DISULEPID	35	74	BY SIMILARITY.	
SQ	SEQUENCE	92 AA:	10170 MW;	BAPBECC2B4208AB6 CR664;	
	Query Match		25.5%;	Score 91.5;	DB 1;
	Best Local Similarity		37.3%;	Pred. No. 0.00019;	
Matches	22;	Conservative	9;	Mismatches	25;
				Indels	3;
				Gaps	2;
QY	6 SPPRCRPFESHVA--RANKVHLKILNTPNCALDQIVARLKNRRNOVCIDPLKWTIOEVL	62			
	1 1 1 1 : 1 1 1 1 : 1 1 : 1 1 1 1 : 1 1 1 1 : 1 1 1 1 :				
29 SDTTPCCFAYLIALPLRAHVKEY-FYTSSKCSNLAVVFVTBRNRNOVCANPEKKWQEYI	86				
RESULT 11					
ID	GRO_MOUSE	STANDARD;	PRT;	96 AA.	
ID	GRO_MOUSE				
CC	p12850;				

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth regulated protein precursor (CXCL1) (Platelet-derived growth factor-inducible protein KC) (Secretory protein N51).
 GN SCYB1 OR GRO1 OR GRO OR MGA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89139485; PubMed=2917992;
 RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
 RT "The platelet-derived growth factor-inducible KC gene encodes a secretory protein related to platelet alpha-granule proteins.";
 RL J. Biol. Chem. 264:4133-4137(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89078502; PubMed=2909392;
 RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
 RT "Cloning and sequence of a secretory protein induced by growth factors in mouse fibroblasts.";
 RL Exp. Cell Res. 180:266-275(1989).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC SPRAIN=129/SV;
 RA Bozic C.R., Kolakowski L.F., Jr., von Duxkull C., Garcia-Rodriguez M., Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96016008; PubMed=7561058;
 RA Ohmori Y., Fukumoto S., Hamilton T.A.;
 RT "Two structurally distinct kappa B sequence motifs cooperatively control LPS-induced KC gene transcription in mouse macrophages.";
 RL J. Immunol. 155:3593-3600(1995).
 CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
 CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: J04596; AAA0131.1; -;
 DR EMBL: U20634; AAB0376.1; -;
 DR EMBL: U20627; AAB0376.1; JOINED.
 DR EMBL: S79767; -; NOT_ANNOTATED_CDS.
 DR PIR: A32954; A32954.
 DR PIR: JH0081; JH0081.
 DR HSSP: P19875; IONK.
 DR MGD: MGI:108068; Gro1.
 DR InterPro: IPR001089; CXK_cmkline_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXK.
 DR SMART: SM00199; SCT; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT CHAIN 1 24 PROBABLE.
 FT DISULFID 33 59 BY SIMILARITY.
 FT DISULFID 33 75 BY SIMILARITY.
 SQ SEQUENCE 96 AA; 10254 MW; 4A52B5EC38B45C2 CRC64;

Query Match 25.5%; Score 91.5; DB 1; Length 96;
 Best Local Similarity 32.8%; Pred. No. 0.00019;
 Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;
 QY 8 RCPGRFFSHVARNVAKHLKIL-NTPNCA-LQIVARKNNRQYCIDPKKIQIETLEKA 65
 DB 32 RCOCLQTMAGIHKKNIQSLKVLPSGPHCTQTEVIATLTK-NGRFACIDPEAPLVQKIVQM 90
 QY 66 L 66
 DB 91 L 91
 RESULT 12
 IL8_MACMU STANDARD; PRT; 101 AA.
 AC P51495;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Macaca mulatta (Rhesus macaque), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544, 9545;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; TISSUE=Blood;
 RX MEDLINE=95353132; PubMed=7628861;
 RA Minnerly J.C., Baganoff M.P., Deppeler C.L., Keller B.T., Rapp S.R., Wlodecki D.L., Frelund D.J., Bolanowski M.A.;
 RT "Identification and characterization of rhesus macaque interleukin-8.";
 RL Interleukin 19:313-331(1995).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U19849; AAA6711.1; -;
 DR EMBL: U19851; AAA6713.1; -;
 DR EMBL: S78555; AAA80141.2; -;
 DR HSSP: P10145; 2IL8.
 DR InterPro: IPR001089; CXK_cmkline_sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXK.
 DR SMART: SM00199; SCT; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.

```

FT  DISUFEID 36 77 BY SIMILARTY
SQ SEQUENCE 101 AA: 11292 MW: 40E8418B57C6A5B CRC64:
Query Match 25.3% Score 91: DB 1: Length 101:
Best Local Similarity 30.4% Pred. No. 0.00024:
Matches 21: Conservative 20: Mismatches 20: Indels 8: Gaps 5:
QY 3 VSLSPRCPRFFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNRRNOYCIDPKLKW 57
   : 11 : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 28 MSTSLRQCC--IKTHSPFHPKFIKELRVISGPHENSELIIVKL-TNGKEVCIDPKKEKW 84
QY 58 IOEYLEKAL 66
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 85 VQKVVQAF 93

RESULT 14
IL8_PIG STANDARD: PRT: 103 AA.
ID IL8_PIG
AC P26894: P22951:
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage
DE chemotactic factor I) (AMCF-1).
GN IL8.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxId=9823:
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103307; PubMed=8276881;
RA Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,
RA Weiss D.J., Murtaugh M.P.;
RT "Regulation of interleukin-8 expression in porcine alveolar
RT macrophages by bacterial lipopolysaccharide.";
RT J. Biol. Chem. 269:77-85(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Sanjanwala M.;
RA Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.
RX TISSUE=Lung;
RX MEDLINE=93041741; PubMed=1420165;
RA Goodman R.B., Foster D.C., Mathewes S.L., Osborn S.G., Kuiper J.L.,
RA Forstrom J.W., Martin T.R.;
RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil
RT chemotactic factors I and II; identification of porcine IL-8 and
RT another intercrine-alpha protein.";
RT Biochemistry 31:10483-10490(1992).
RN [4]
RP REVISION TO 23.
RA Goodman R.B.;
RX Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 26-45.
RX STRAIN=Yorkshire;
RX MEDLINE=91217086; PubMed=1850745;
RA Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;
RT "Identification of two neutrophil chemotactic peptides produced by
RT porcine alveolar macrophages.";
RT J. Biol. Chem. 266:8455-8463(1991).
RN [6]
RP FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
RP BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
RP NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
RP RESPONSE TO AN INFLAMMATORY STIMULUS.
RN [7]
RP SUBUNIT: HOMODIMER.
RN [8]
RP TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.
RN [9]
RP INDUCTION: BY LIPOLYSACCHARIDE (LPS).
RN [10]
RP SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
RN C-X-C) (CHEMOKINE CXCL).

```

```

-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M86923; AAA16616.1; -
DR EMBL: X61151; CAA43461.1; -
DR EMBL: M9367; AAA92576.1; -
DR PIR: A44253; A44253.
DR PIR: A39819; A39819.
DR HSSP: P10145; 1IKM.
DR InterPro: IPR001089; CXC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00437; SMALL_CYTOKINE_CXC.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 25
FT CHAIN 26 103 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
FT CONFLICT 33 34 RC -> CR (IN REF. 5).
FT CONFLICT 87 87 K -> KK (IN REF. 2).
SQ SEQUENCE 103 AA; 11633 MW; 9FE0E350E1928C64 CRC64;

Query Match 25.1%; Score 90; DB 1; Length 103;
Best Local Similarity 31.8%; Pred. No. 0.00032;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

OY 3 VSPPCPCRFESHVARAN---VKHLKIITNT-PNCA-LQIVARLKNNNROVCIIDPKIKW 57
DB 28 VSAELKQCQ--INTHSTPRPKFKELRVIESGPHCENSEITVLYV-NGKEVCLDPKRW 84
OY 58 IOEYLE 63
DB 85 VQKVVO 90

RESULT 15
SY05_CAVPO STANDARD; PRT; 91 AA.
AC P97272; O09076;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
DE protein) (SIS-delta).
GN SCYA5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Dunkin-Hartley;
RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B.,
RA Wells T.N.C., White A.M., Westwick J., Watson M.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A.,
RA Yamaguchi K., Kanazawa M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.

```

```

-----
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U77037; AAC53293.1; -
DR EMBL: AB002662; BAA19604.1; -
DR HSSP: P13501; 1RTN.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 23
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
SQ SEQUENCE 91 AA; 10088 MW; 7F6A31B751237DB9 CRC64;

Query Match 24.7%; Score 88.5; DB 1; Length 91;
Best Local Similarity 33.3%; Pred. No. 0.00043;
Matches 20; Conservative 14; Mismatches 21; Indels 5; Gaps 3;

OY 6 SPSPCPCRFESHVARANVK-HLK--ILNTPNCALQIVARLKNNNROVCIIDPKIKWIOEYL 62
DB 28 SPTTPCCF--AVYSRALPRTHIKEYFTSSKCSNLAVFVTRKNRQVCANPEKKWREYI 85

Search completed: January 23, 2003, 15:34:19
Job time : 6 secs

```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 : Search time 22.6 Seconds
(without alignments)
610.848 Million cell updates/sec

Title: US-09-852-424-4
Perfect score: 359
Sequence: 1 KGVSLSPRCPCRFESHVAR.....QVCIDPKLKIQETLEKALN 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriap:*
17: SP-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	341	95.0	92	4	Q9H554
2	333	92.8	89	11	Q9QZD1
3	275	76.6	94	13	Q8UJ99
4	94.5	26.3	91	11	Q91ZL1
5	88	24.5	98	13	Q8QCV8
6	88	24.5	109	13	Q8QV59
7	84.5	23.5	134	12	Q9YVA9
8	84.5	23.5	142	12	Q91B37
9	84	23.4	203	12	Q67634
10	81.5	22.7	97	13	Q8QF55
11	81	22.6	95	12	Q98158
12	81	22.6	104	13	Q73912
13	79.5	22.1	97	11	Q9Z318
14	79.5	22.1	101	11	Q93442
15	79.5	22.1	108	6	Q28724
16	79	22.0	79	4	Q95689

17	79	22.0	148	11	Q9QYD7	Q9QYD7 mus musculus
18	77.5	21.6	363	13	Q9QZT0	Q9QZT0 brachydanio
19	77.5	21.6	1096	13	Q9QZT1	Q9QZT1 brachydanio
20	77	21.4	97	13	Q98702	Q98702 oncorhynch
21	76.5	21.3	100	11	Q91ZK9	Q91ZK9 sigmodon hi
22	76.5	21.3	101	11	Q91ZK9	Q91ZK9 sigmodon hi
23	76	21.2	101	13	Q8UW91	Q8UW91 tritakis scf
24	76	21.2	106	11	Q9Z292	Q9Z292 cricetus
25	73.5	20.5	126	11	Q99360	Q99360 mus musculus
26	73.5	20.5	883	13	Q91493	Q91493 torpedo cal
27	73	20.3	102	6	Q95M27	Q95M27 ovis aries
28	72.5	20.2	89	13	Q918E0	Q918E0 gallus gall
29	71.5	19.9	601	13	Q73928	Q73928 scyllorhinu
30	70.5	19.6	91	13	Q8QGS6	Q8QGS6 gallus gall
31	70.5	19.6	97	6	Q9TTS6	Q9TTS6 bos taurus
32	70	19.5	80	4	Q14745	Q14745 homo sapien
33	70	19.5	91	13	Q8QGS7	Q8QGS7 gallus gall
34	70	19.5	92	6	Q8S040	Q8S040 felis silve
35	69.5	19.4	100	6	Q9TTO4	Q9TTO4 equus caball
36	69	19.2	93	4	Q96168	Q96168 homo sapien
37	69	19.2	96	13	Q90825	Q90825 gallus gall
38	69	19.2	395	11	Q91V44	Q91V44 mus musculus
39	67.5	18.8	116	11	Q91ZB2	Q91ZB2 mus musculus
40	67.5	18.8	150	11	Q9QW66	Q9QW66 mus sp. dys
41	67.5	18.8	258	11	Q9D6J7	Q9D6J7 mus musculus
42	67.5	18.8	622	4	Q02295	Q02295 homo sapien
43	67.5	18.8	3685	4	Q14205	Q14205 homo sapien
44	66.5	18.5	101	11	Q9EP62	Q9EP62 ratius norv
45	66	18.4	92	11	Q91Z65	Q91Z65 sigmodon hi

ALIGNMENTS

RESULT 1
ID Q9H554 PRELIMINARY: PRT: 92 AA.
AC Q9H554:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)
DE (Fragment).
GN SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137026; CAC10202.1; -.
DR HSSP; P48061; 1SDP.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
FT NON_TER
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B44EBD20 CRC64;

Query Match 95.0%; Score 341; DB 4; Length 92;
Best Local Similarity 97.0%; Pred. No. 7.4e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0;

QY	1	KGVSLSPRCPCRFESHVARANKHLINTPGCAIQIVARLKNRRQVCIDPKLKIOWE 60
DB	22	KVSLSPRCPCRFESHVARANKHLINTPGCAIQIVARLKNRRQVCIDPKLKIOWE 81
QY	61	YLEKALN 67
DB	82	YLEKALN 88

SO	SEQUENCE	98 AA	10846 MW	495CA839A5D8C92	CRC64
QY	Query Match	24.5%	Score 88	DB 13	Length 98
Db	Best Local Similarity	31.9%	Pred. No. 0.0022		
Matches	22	Conservative 17	Mismatches 24	Indels 6	Gaps 4
QY	2 GVSISPRCPGFFESHVARANVKHLKILNTPN-C-ALQIYARLKNNRNOVCIDPKLMI 58				
Db	30 GVSLL-HCRCTETESRPIGRYIKSVETI-SPNSHCDKTEITATLKDVGVELCLDPEAPWV 86				
QY	59 QEYLEKALN 67	::: ::			
Db	87 KRVINKLIS 95	::: ::			
RESULT 6					
Q90YV59	PRELIMINARY	PRT	109 AA.		
AC	Q90YV59				
DT	01-DEC-2001 (TREMBLREL. 19, Created)				
DT	01-DEC-2001 (TREMBLREL. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLREL. 20, Last annotation update)				
DE	Interleukine-8.				
GN	IL-8.				
OS	Paralichthys olivaceus (Flounder).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;				
OC	Pleuronectidae; Paralichthyidae; Paralichthys.				
OX	NCBI_Taxid=8255;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21435923; PubMed=11551708;				
RA	Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;				
RT	"Cloning and sequence analysis of the Interleukin-8 gene from flounder				
RT	(Paralichthys olivaceus).";				
RL	Gene 274:237-243(2001);				
DR	EMBL; AF216646; AAL05442.1; -				
DR	InterPro; IPR001811; Chemokine_IL8.				
DR	Pfam; PF00048; IL8; 1.				
SO	SEQUENCE 109 AA; 12117 MW; C7CE1896C50A6ED CRC64;				
QY	Query Match	24.5%	Score 88	DB 13	Length 109
Db	Best Local Similarity	31.9%	Pred. No. 0.0025		
Matches	22	Conservative 17	Mismatches 24	Indels 6	Gaps 4
QY	2 GVSISPRCPGFFESHVARANVKHLKILNTPN-C-ALQIYARLKNNRNOVCIDPKLMI 58				
Db	29 GVSLL-HCRCTETESRPIGRYIKSVETI-SPNSHCDKTEITATLKDVGVELCLDPEAPWV 85				
QY	59 QEYLEKALN 67	::: ::			
Db	86 KRVINKLIS 94	::: ::			
RESULT 7					
Q9YVA9	PRELIMINARY	PRT	134 AA.		
AC	Q9YVA9				
DT	01-MAY-1999 (TREMBLREL. 10, Created)				
DT	01-MAY-1999 (TREMBLREL. 10, Last sequence update)				
DT	01-JUN-2002 (TREMBLREL. 21, Last annotation update)				
DE	VIL8 (CXC chemokine VIL8).				
GN	MDV003 OR MDV078.				
OS	Gallid herpesvirus 1.				
OS	Marck's disease herpesvirus (strain GA) (MDHV), and				
OS	Marck's disease herpesvirus (strain Md5) (MDHV), Turkey herpesvirus.				
OC	Vitruex; dsDNA viruses, no RNA stage; Herpesviridae;				
OC	Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.				
OX	NCBI_Taxid=10386, 10388, 10389;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=galid herpesvirus 1; STRAIN=RB1B;				

```

RA Rassaert D., Fragnet L.; "Characterisation of the Marek's disease virus RT RB18 strain (serotype I)." ; RA submitted (DEC-2000) to the EMBL/GenBank/DBJ databases. RN [2] RP SEQUENCE FROM N.A. RC SPECIES=Marek's disease herpesvirus (strain GA) (MDHV); RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.; "CXG chemokine encoded by Marek's Disease Virus (MDV)."; RT Submitted (May-1998) to the EMBL/Genbank/DBJ databases. RN [3] RP SEQUENCE FROM N.A. RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV); RX MEDLINE=20392152; PubMed=10933706; RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.; "The genome of a very virulent Marek's disease virus." ; RL J. Virol. 74:7980-7988(2000). RN [4] RP SEQUENCE FROM N.A. RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV); RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.; RL submitted (MAR-2000) to the EMBL/Genbank/DBJ databases. DR EMBL: AF311499; AAL58097.1; - DR EMBL: AF065430; AAC77449.1; - DR EMBL: AE243438; AAG14290.1; - DR EMBL: AF243438; AAG14256.1; -. DR HSSP: P10889; IMI2. DR InterPro: IPRO01811; Chemokine_IL8. DR InterPro: IPRO01089; CXCL_chem_kine_smll. DR Pfam: PF00048; IL8; 1. DR PRINTS: PRO0437; SMALLCYTCKXC. DR SMART: SM00199; SCY; 1. SQ SEQUENCE 134 AA; 14828 MW; CB59CDB86BD25190 CRC64;

Query March          23.5%; Score 84.5; DB 12; length 134;
Best Local Similarity   25.9%; Pred No. 0.0083;
Matches    22; Conservative    14; Mismatches     12; Indels      37; Gaps

Qy       2 GVSL-----SPRCPCRFESHVARANVKHLILNTP-----NC-AIQIV 39
           |||         || |        :|||         :|||         :|||
Db       22 GISLSLAVDKRNKC-----VKVTNPRTGLGIPLAVDIVPGIHCRRETI 67

Qy       40 ARLKNNRQCVIDPKLNIOEYLEK 64
           |||         |||         :|||||        :||:::||
Db       68 FALK-KNRKVGVDPAPWQQPFIKK 91

RESULT 8
Q9IBJ7 PRELIMINARY;             PRT;            142 AA.
AC Q9IBJ7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DD 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE VIL-8.
GN R-LORF2.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Alphaherpesvirinae; Marek's disease-like viruses.
CX NCBI_TaxID=10390;
CN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-GA: MEDLIN=92237304; PubMed=1315048;
RA Jones D., Lee L., Liu J.L., Kung H.J., Tilletson J.K.:
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
the fos/jun oncogenes that is highly expressed in lymphoblastoid
tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992). RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-GA: Lee L.F., Wu P., Sul D., Ren D., Kung H.J.;
```

RT "The Complete UL Sequence of Serotype I Marek's Disease Virus."
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
 DR EMBL: AF147806; AAF67205.1; -
 DR EMBL: AF147806; AAF6793.1; -
 DR HSSP: P10889; 1MI2
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12; Chemokine-sm1.
 DR InterPro: IPR001230; Prey11-site.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCKC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00294; PRENATION; UNKNOWN_1.
 SQ SEQUENCE 142 AA; 15770 MW; 35ABCEB9B29FD209 CRC64;
 Query Match 23.5%; Score 84.5; DB 12; Length 142;
 Best Local Similarity 25.9%; Pred. No. 0.0088;
 Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps 5;
 QY 2 GVSF-----SPRCPREFESHVARANKHLKILNTP-----NC-ALQIV 39
 DB 22 GISLESLAVDKRC-----VKVTRPTGLIIVADVIPIGTHCRREII 67
 QY 40 ARKNNRQVCIDPKLKWIOEYLEK 64
 DB 68 FALK-KNRKVCVDEAPVVOOFIRK 91

RESULT 9

ID 067634 PRELIMINARY; PRT; 203 AA.
 AC 067634;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Eco Q protein (Fragment).
 OS Marek's disease herpesvirus (strain GA) (MDHV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 NCBI_TaxID=10388;
 RX MEDLINE=96074534; PubMed=7491783;
 RA Peng Q., Zeng M., Bhuiyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
 RA Shirazi Y.;
 RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
 RT mapping to the BamHI-12, BamHI-02, and BamHI-L fragments of the MDV
 RT genome from lymphoblastoid cells transformed and persistently infected
 RT with MDV."
 RL Virology 213:590-599(1995).
 DR EMBL: U34966; AAC54629.1; -
 DR HSSP: P10889; 1MI2
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL12; Chemokine-sm1.
 DR InterPro: IPR004827; TF_PZIP.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCKC.
 DR SMART: SM00338; BRIZ; 1.
 DR SMART: SM00199; SCY; 1.
 DR SMART: SM00199; SCY; 1.
 FT NON_TER 1
 SQ SEQUENCE 203 AA; 23132 MW; DE42F2A1C1A71C88 CRC64;

Query Match 23.4%; Score 84; DB 12; Length 203;
 Best Local Similarity 23.5%; Pred. No. 0.015;
 Matches 19; Conservative 17; Mismatches 13; Indels 32; Gaps 4;

QY 1 KGVSLSPRCPCREFESHVARANKHLKILNTP-----NC-ALQIVARLK 43
 DB 95 ESILAVDKRC-----VKVTRPTGLIIVADVIPIGTHCRREII 140
 QY 44 NNRQVCIDPKLKWIOEYLEK 64
 DB 141 -KNRKVCVDEAPVVOOFIRK 160

RESULT 10

ID 080FP5 PRELIMINARY; PRT; 97 AA.
 AC 080FP5;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE CXC chemokine.
 GN CXC CHEMOKINE.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 NCBI_TaxID=7962;
 RX MEDLINE=97121480; PubMed=8962146;
 RA Russo J.J., Bohenkky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
 RT (HHV-8)."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
 FT [3]
 SQ SEQUENCE FROM N.A.
 RA Russo J.J., Bohenkky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 SQ SEQUENCE FROM N.A.

Query Match 22.7%; Score 81.5; DB 13; Length 97;
 Best Local Similarity 31.0%; Pred. No. 0.014;
 Matches 22; Conservative 16; Mismatches 28; Indels 5; Gaps 2;

QY 1 KGVSLSPRCPCREFESHVARANKHLK-----INTPCALQ-IVARLNNRQVCIDPKL 55
 DB 19 KGQARARKGCFVCVKNNVPPKQIKELIPASRCKTQELIVTLKSTEDKCLNPES 78
 QY 56 KWIQEVLEKAL 66
 DB 79 KFTQKYMKAIV 89

RESULT 11

ID 098158 PRELIMINARY; PRT; 95 AA.
 AC 098158; 012569;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ORF K6.
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 NCBI_TaxID=37296;
 RX MEDLINE=97094384; PubMed=8939871;
 RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
 RT "Molecular mimicry of human cytokine and cytokine response pathway
 RT genes by KSHV."
 RL Science 274:1739-1744(1996).
 FT [2]
 SQ SEQUENCE FROM N.A.
 RA Russo J.J., Bohenkky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 SQ SEQUENCE FROM N.A.

RA Nicholas J., Ruvoletto V.R., Burns W.H., Sandford G., Wan X., Clufo D.,
 RA Hendrickson S., Guo H.C., Hayward G.S., Reitz M.S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Russo J.D., Bohanzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97296220; PubMed-9151804;
 RA Neipel F., Albrecht J.C., Fleckenstein B.;
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
 RT human herpesvirus 8: determinants of its pathogenicity?";
 RL J. Virol. 71:4187-4192(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Sun R., Lin S.-F., Miller G.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Ren S., Lin S.-F., Miller G.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U75698; AAC57095.1; -;
 DR EMBL: U74585; AAB61704.1; -;
 DR EMBL: U93872; AAB62671.1; -;
 DR EMBL: U71366; AAC34943.1; -;
 DR EMBL: U50138; AAD11536.1; -;
 DR HSSP: Q98157; IYMP.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 95 AA; 10485 MW; 34B9AFC4987FC485 CRC64;

Query Match 22.6%; Score 81; DB 12; Length 95;
 Best Local Similarity 25.8%; Pred. No. 0.016;
 Matches 16; Conservative 11; Mismatches 35; Indels 0; Gaps 0;
 Oy 3 VLSLPRCGRFESHVARANKHLKILNTPMCAQIYARLKNNRQVCIDPKLWIOEYL 62
 Db 29 VSYPNSCVYFOQHPPVQILKEWYPTSPACPKPGVILLTRGRQICADPSKNMVRQLM 88
 Oy 63 EK 64
 Db 89 QR 90
 RESULT 12
 ID 073912 PRELIMINARY; PRT; 104 AA.
 AC 073912;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE K60 protein precursor (CXC chemokine K60).
 CN K60.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MACROPHAGE LIKE;
 RA Slick C.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20170941; PubMed-10704244;
 RA Slick C., Schneider K., Staeheli P., Wehling K.C.;
 RT "Novel chicken CXC and CC chemokines.";
 RT Cytokine 12:181-186(2000).

RN [3]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RT "Mapping of a second EIR CXC chemokine to chicken chromosome four.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y14971; CAA75212.1; -;
 DR EMBL: AF277660; AAF6485.1; -;
 DR HSSP: P02775; IYVX.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXC-chemokine-sm1.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 104 K60 PROTEIN.
 SQ SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;
 Query Match 22.6%; Score 81; DB 13; Length 104;
 Best Local Similarity 29.2%; Pred. No. 0.017;
 Matches 19; Conservative 18; Mismatches 20; Indels 8; Gaps 4;
 Oy 8 RCPGRFESHVARANKHLKILNT---PNCA-LQIVARLKNNRQVCIDPKLWIOEYL 62
 Db 33 RQCC--LETHSKFHPRKIQNVNLTSPSGPHCKNVEVIAFLK-DGREVCCLDPTAPVVKLLI 89
 Oy 63 EKALN 67
 Db 90 KALID 94

RESULT 13
 ID Q92318 PRELIMINARY; PRT; 97 AA.
 AC Q92318;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Monocyte chemoattractant protein-3 (MCP-3).
 OS Cavia porcellus (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognathii; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,
 RA Ishizaka A., Yamaguchi K., Kanazawa M.;
 RT "Differential expression of CC chemokines in guinea pig lungs during
 RT an allergic inflammation.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB014340; BAA36456.1; -;
 DR HSSP: P51671; IEOT.
 DR InterPro: IPR000827; CC-chemokine-sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;
 Query Match 22.1%; Score 79.5; DB 11; Length 97;
 Best Local Similarity 30.3%; Pred. No. 0.025;
 Matches 20; Conservative 13; Mismatches 28; Indels 5; Gaps 2;
 Oy 2 GVSLSPRCGRFESHVARANKHLKILNTPMCAQIYARLKNNRQVCIDPKLWIOEYL 60
 Db 27 GVNITSCYKRSQRIRVR--LESTRTITSSKCPQWAVIFKTKFKREICADPKQWVDS 84
 Oy 61 --YLEK 64
 Db 85 MKYIDK 90

```

RESULT 14
O93442 PRELIMINARY; PRT; 101 AA.
ID 093442
AC 093442
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE LFCA-1 protein precursor.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxId=7746;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEUKOCYTES;
RA Najash A.M., Mechelina L.V., Alabyev B.Y., Tarantin A.V.;
RT "Identification of the interleukin 8 homologue in lamprey (Lampetra
RT fluviatilis): early evolutionary divergence of chemokines.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ231072; CAA13114.1; -.
DR HSSP: P02775; ITVX.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL_chemokine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1.
KW Signal.
KM SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT CHAIN 23 101 LFCA-1 PROTEIN.
SQ SEQUENCE 101 AA; 11095 MW; 80CFE81EA7336D2 CRC64;

Query Match
Best Local Similarity 26.9%; Score 79.5; DB 13; Length 101;
Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;

OY 8 RCPCFEESHVAVANV-KHLK---ILNTPNCA-LQIVARLKNRRQVCIDPKLWQEVLEKA 60
DB 30 RCQC-----VHISKFIHPKHFTMEVYIPQSSNCKNVEIIVTMKSTNNQICLNDAPWVRK 85
OY 61 YLEKALN 67
DB 86 VISHILD 92

```

```

RESULT 15
O28724 PRELIMINARY; PRT; 108 AA.
ID 028724
AC 028724
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1999 (TREMBLrel. 11, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE GRO (Permeability factor 2).
GN RPF2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RA Yoshimura T., Modi W.S.;
RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXCL
RT chemokine subfamily in mammals.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 43-108 FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RX MEDLINE=95129889; PubMed=7828903;
RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA Martin T.R.;
RT "Cloning of two rabbit GRO homologues and their expression in alveolar
RT macrophages.";

```

```

RL Gene 151:337-338(1994).
DR EMBL: U95808; AAB93924.1; -.
DR EMBL: L28933; AAB66975.1; -.
DR HSSP: P19875; 10NK.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL_chemokine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5B4D CRC64;

Query Match
Best Local Similarity 27.4%; Score 79.5; DB 6; Length 108;
Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

OY 8 RCPCFEESHVAVANV-KHLKILNT-PNCA-LQIVARLKNRRQVCIDPKLWQEVLEKA 65
DB 43 RCQCLOTVGCHLKSISQSLKVLSPGPHCAQTEVIATLK-SGQACLNPAAPWVKRFLQKR 101
OY 66 LN 67
DB 102 LS 103

```

Search completed: January 23, 2003, 15:36:20
Job time : 22.6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:27:48 : Search time 28.2 seconds
(without alignments)
316.568 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361
Sequence: 1 KGVSLSTPCPCRFESHVAR.....QVCIDPKLKIQVLEKALN 67

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	100.0	67	23	AAW48660
2	352	97.5	67	23	AAW48656
3	347	96.1	67	23	AAW48658
4	345	95.6	67	23	AAW48657
5	344	95.3	67	19	AAW50760
6	344	95.3	67	20	AAV34092
7	344	95.3	67	20	AAV06741
8	344	95.3	67	20	AAV06726
9	344	95.3	67	21	AAV67594
10	344	95.3	67	23	AAW47680

11	344	95.3	68	19	AAW50761
12	344	95.3	69	20	AAV05818
13	344	95.3	72	19	AAW50762
14	344	95.3	72	20	AAV34093
15	344	95.3	72	21	AAV67595
16	344	95.3	73	19	AAW50763
17	344	95.3	73	20	AAV05819
18	344	95.3	74	21	AAV69041
19	344	95.3	89	16	AAW75419
20	344	95.3	89	20	AAV39959
21	344	95.3	89	20	AAV26177
22	344	95.3	89	21	AAW5791
23	344	95.3	89	21	AAV93603
24	344	95.3	89	21	AAV52508
25	344	95.3	90	20	AAV05820
26	344	95.3	93	16	AAW75420
27	344	95.3	93	19	AAW50766
28	344	95.3	93	20	AAV26178
29	344	95.3	93	20	AAV06725
30	344	95.3	93	21	AAW15812
31	344	95.3	93	23	AAE23952
32	344	95.3	93	23	AAW84305
33	344	95.3	93	23	AAW47690
34	344	95.3	93	23	AAW47691
35	344	95.3	94	20	AAV05821
36	344	95.3	101	23	AAW48051
37	344	95.3	119	23	AAW48047
38	344	95.3	166	20	AAV29899
39	344	95.3	177	20	AAV29896
40	344	95.3	320	21	AAV69055
41	344	95.3	322	21	AAV69056
42	344	95.3	326	19	AAW76221
43	344	95.3	327	21	AAV69057
44	344	95.3	328	19	AAW76220
45	344	95.3	339	20	AAV29905

ALIGNMENTS

RESULT 1					
AAW48660	ID	AAW48660	standard; peptide; 67 AA.		
XX	AC	AAW48660;			
XX	XX				
DT	20-MAY-2002	(first entry)			
XX	XX				
DE	XX	XX			
XX	XX	XX			
XX	XX	XX			
OS	Synthetic.				
XX	XX				
XX	XX				
FT	Key	Location/Qualifiers			
FT	Modified-site	8			
FT	FT	/note="Optionally the proline analogue 6-amino-7-oxo-2,3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic acid residue"			
FT	FT				
XX	XX				
PN	WO200185196-A2.				
XX	XX				
PD	15-NOV-2001.				
XX	XX				
PF	09-MAY-2001; 2001WO-CA00659.				
XX	XX				
PR	09-MAY-2000; 2000CA-2305787.				
PR	19-MAY-2000; 2000US-205467P.				
XX	XX				
PA	(UVR-) UNIV BRITISH COLUMBIA.				
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.				

Peptide which bind
N-terminal modifie
Peptide which bind
Native stromal cel
SDF-beta peptide
Peptide which bind
N-terminal modifie
Amino acid sequenc
Human SDF-1-alpha.
Human SDF-1-alpha
Stromal cell deriv
Human chemokine SD
A human B-cell sti
Human stromal cell
N-terminal modifie
Human SDF-1-beta.
Human SDF-1 which
Stromal cell deriv
Amino acid sequenc
Human chemokine SD
Human chemokine SD
Human endometrial
SDF-1 precursor.
SDF-1-beta. Homo
N-terminal modifie
SDF-1gamma SEQ. ID
Human SDF-1gamma S
Human SDF-1 beta a
Human SDF1 and hum
A chemokine recept
A chemokine recept
Human chemokine SD
A chemokine recept
Human chemokine SD
Human SDF-1 and hu

XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 XX
 XX
 DR WPI; 2002-106073/14.
 XX
 PT Promoting the rate of haematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 XX
 PS Claim 9; Page 54; 68pp; English.
 CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 CC
 XX
 SQ Sequence 67 AA;
 Query Match 100.0%; Score 361; DB 23; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1e-39;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGVSLSTPCPCRFESHVARANWKHLKILNTPNCALQIVARLKNNNRQVCIDPRKLKIQE 60
 Db 1 KGVSLSTPCPCRFESHVARANWKHLKILNTPNCALQIVARLKNNNRQVCIDPRKLKIQE 60
 QY 61 YLEKALN 67
 Db 61 YLEKALN 67
 Db 61 YLEKALN 67
 RESULT 2
 AAM48656
 ID AAM48656 standard; peptide; 67 AA.
 AC AAM48656;
 XX
 XX 20-MAY-2002 (first entry)
 DT
 XX CXCR4 peptide antagonist SEQ ID NO 1.
 DE
 XX CXCR4; haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KM cell multiplication.
 XX
 OS Synthetic.
 XX
 PN WO200185196-A2.
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001; 2001WO-CA00659.
 XX
 PR 09-MAY-2000; 2000CA-2305787.
 PR 19-MAY-2000; 2000US-205467P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 XX
 DR WPI; 2002-106073/14.
 XX
 PT Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 XX
 PS Claim 9; Page 54; 68pp; English.
 CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 CC
 XX
 SQ Sequence 67 AA;
 Query Match 97.5%; Score 352; DB 23; Length 67;
 Best Local Similarity 98.5%; Pred. No. 1.6e-38;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KGVSLSTPCPCRFESHVARANWKHLKILNTPNCALQIVARLKNNNRQVCIDPRKLKIQE 60
 Db 1 KGVSLSTPCPCRFESHVARANWKHLKILNTPNCALQIVARLKNNNRQVCIDPRKLKIQE 60
 QY 61 YLEKALN 67
 Db 61 YLEKALN 67
 Db 61 YLEKALN 67
 RESULT 3
 AAM48658
 ID AAM48658 standard; peptide; 67 AA.
 AC AAM48658;
 XX
 XX 20-MAY-2002 (first entry)
 DT
 XX CXCR4 peptide antagonist SEQ ID NO 3.
 DE
 XX CXCR4; haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KM cell multiplication.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "optionally the proline analogue 6-amino-7-oxo-2,
 FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
 FT acid residue or a bicyclic turned dipeptide
 FT (Btd)"
 XX
 PN WO200185196-A2.
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001; 2001WO-CA00659.
 XX
 PR 09-MAY-2000; 2000CA-2305787.
 PR 19-MAY-2000; 2000US-205467P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 XX
 DR WPI; 2002-106073/14.
 XX
 PT Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 XX
 PS Claim 9: Page 54; 68pp; English.
 XX
 CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 XX
 SQ Sequence 67 AA:
 Query Match 96.1%; Score 347; DB 23; Length 67;
 Best Local Similarity 97.0%; Pred. No. 7e-38; 2; Indels 0; Gaps 0;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGVSLSPGCPREFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 DB 1 KGVSLSPGCPREFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 4
 AAM48657
 ID AAM48657 standard; peptide: 67 AA.
 AC AAM48657;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE CXCR4 peptide antagonist SEQ ID NO 2.
 XX
 KW CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.
 XX
 OS Synthetic.
 XX
 FI Key Location/Qualifiers
 FT Modified-site 5 /note="Optionally the proline analogue 6-amino-7-oxo-2,
 FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic
 FT acid residue or a bicyclic turned dipeptide
 FT (Btd)"
 XX
 PN WO200105196-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001: 2001WO-CA00659.
 XX
 PR 09-MAY-2000: 2000CA-2305787.
 PR 19-MAY-2000: 2000US-205467P.
 XX
 PA (UVR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Sallat H;
 XX
 DR WPI: 2002-106073/14.
 PT Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the
 PT cells -
 XX
 PS Claim 9: Page 54; 68pp; English.
 XX
 CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the haematopoietic cells in a patient; for
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.
 XX
 SQ Sequence 67 AA:
 Query Match 95.6%; Score 345; DB 23; Length 67;
 Best Local Similarity 97.0%; Pred. No. 1.3e-37; 2; Indels 0; Gaps 0;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGVSLSPGCPREFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 DB 1 KGVSLSPGCPREFESHVARANKHLKILTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 5
 AAM50760
 ID AAM50760 standard; peptide: 67 AA.
 AC AAM50760;
 XX
 DT 27-JUL-1998 (first entry)
 XX
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
 XX
 KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
 XX
 OS Homo sapiens.
 XX
 PN FR2751658-A1.
 XX
 PD 30-JAN-1998.
 XX
 PF 26-JUL-1996; 96FR-0009477.
 PF 26-JUL-1996; 96FR-0009477.
 PR 26-JUL-1996; 96FR-0009477.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
 PI WPI: 1998-123039/12.
 XX
 DR Human stromal cell-derived chemokine, SDF-1 - useful for treating
 PT human immunodeficiency virus infection
 XX
 PS Claim 2: Page 29; 48pp; French.
 XX
 CC The invention relates to peptides which bind to a cellular receptor for
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-
 CC expressed transmembrane domain receptor), especially where the
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or
 CC prevent HIV infections, optionally together with reverse transcriptase
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-

CC associated opportunistic infections and/or other CXc or CC chemokines,
CC especially RANTES, MIP1- alpha , MIP1- beta or MCP1. The peptide can be
CC used to detect anti-SDF-1 antibodies in biological fluids. This
CC sequence represents a specifically claimed peptide which binds to the
CC CXCR4 receptor.

XX
SQ Sequence 67 AA:

Query Match 95.3%; Score 344; DB 19; Length 67;
Best Local Similarity 97.0%; Pred. No. 1,7e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KPSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 6
AAV34092
ID AAV34092 standard; protein; 67 AA.

XX
AC AAV34092;

XX
DT 29-NOV-1999 (first entry)

XX
DE Native stromal cell derived factor 1 (SDF-1) alpha protein.

XX CXc chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
KM Interferon gamma; autoimmune disease; multiple sclerosis; cancer;
KM angiogenesis; stromal cell derived factor 1; SDF-1.

XX
OS Mammalia.

XX
PN WO947158-A2.

XX
PD 23-SEP-1999.

XX
PF 12-MAR-1999; 99WO-CA00221.

XX
PR 13-MAR-1998; 98CA-2226391.

XX
PR 14-AUG-1998; 98CA-2245224.

XX
PA (UYBR-) UNIV BRITISH COLUMBIA.

XX
PI Clark-Lewis I, Gong J, Duronio V;

XX
DR WPI; 1999-561857/47.

XX
PT Use of CXc chemokine receptor 4 for treating autoimmune disease and
PT cancer

XX
PS Example 1; Fig 1; 71pp; English.

XX
CC The invention relates to the use of a CXc chemokine receptor 4 (CXCR4)
CC antagonist for the manufacture of a medicament for reducing interferon
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
CC to treat or to design a medicament to treat, an autoimmune disease,
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
CC antagonists may be peptide compounds comprising a substantially purified
CC peptide fragment, analogue or a pharmacologically acceptable salt of
CC stromal cell derived factor 1 (SDF-1). The present sequence represents
CC the amino acid sequence of SDF-1 alpha protein.

XX
SQ Sequence 67 AA:

Query Match 95.3%; Score 344; DB 20; Length 67;
Best Local Similarity 97.0%; Pred. No. 1,7e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KPSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 7
AAV06741
ID AAV06741 standard; protein; 67 AA.

XX
AC AAV06741;

XX
DT 18-JUN-1999 (first entry)

XX
DE SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;
KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;
KM stromal cell derived factor 1; Macrophage inflammatory protein.

XX
OS Synthetic.
OS Homo sapiens.

XX
PN WO9911655-A1.

XX
PD 11-MAR-1999.

XX
PF 31-AUG-1998; 98WO-US18096.

XX
PR 04-SEP-1997; 97US-0057620.

XX
PA (GRYP-) GRYPHON SCI.

XX
PI Kent SBH, Siani MA, Simon R, Wilken J;

XX
DR WPI; 1999-205128/17.

XX
PT New cross-over proteins for treatment of inflammation and infections
PT e.g. AIDS - prepared by ligation of two functional protein modules
PT derived from two different parent molecules

XX
PS Example 4; Page 43; 75pp; English.

XX
CC The invention relates to a cross-over protein produced by chemical
CC ligation of at least two functional protein modules derived from at
CC least two parent protein molecules. The cross-over proteins can be used
CC in pharmaceutical compositions for therapy of inflammatory and
CC infectious diseases including AIDS, and for indications of hematopoiesis
CC and chemoprotection. They are also useful for treatment of asthma,
CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library
CC comprising a collection of cross-over proteins is useful for screening
CC for cross-over proteins that are receptor ligands. The libraries
CC comprise functionally diverse compounds therefore improving the drug
CC discovery process. The proteins and libraries are exemplified by the
CC preparation of cross-over chemokines comprising various combinations of
CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor
CC 1), VMP (viral Macrophage inflammatory protein) and other such
CC chemokines. Sequences AAV06741-62 represent amino acid sequences of SDF-1
CC alpha/RANTES cross-over molecules.

XX
SQ Sequence 67 AA:

Query Match 95.3%; Score 344; DB 20; Length 67;
Best Local Similarity 97.0%; Pred. No. 1,7e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB 1 KPSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 8
 AAY06726
 ID AAY06726 standard; protein; 67 AA.

XX AAY06726;

DT 18-JUN-1999 (first entry)

DE Amino acid fragment of SDF-1 alpha.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
 KW infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; vmiP;
 KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV;
 KW stromal cell derived factor 1; Macrophage Inflammatory protein.

OS Homo sapiens.
 OS Synthetic.

PN WO9911655-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

PI Kent SBH, Stanl MA, Simon R, Wilken J;

DR WPI: 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections
 PT e.g. AIDS - prepared by ligation of two functional protein modules
 PT derived from two different parent molecules

XX Example 4: Page 41; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical
 CC ligation of at least two functional protein modules derived from at least
 CC two parent protein molecules. The cross-over proteins can be used in
 CC pharmaceutical compositions for therapy of inflammatory and infectious
 CC diseases including AIDS, and for indications of hematopoiesis and
 CC chemoprotection. They are also useful for treatment of asthma, allergic
 CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library
 CC comprising a collection of cross-over proteins is useful for screening
 CC for cross-over proteins that are receptor ligands. The libraries comprise
 CC functionally diverse compounds therefore improving the drug discovery
 CC process. The proteins and libraries are exemplified by the preparation
 CC of cross-over chemokines comprising various combinations of peptide
 CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), vmiP
 CC (viral Macrophage Inflammatory protein) and other such chemokines. The
 CC present sequence represents an amino acid fragment of SDF-1 alpha which
 CC acts as a synthetic base molecule for synthesizing the cross-over
 CC protein.

XX Sequence 67 AA:

Query Match 95.3%; Score 344; DB 20; Length 67;
 Best Local Similarity 97.0%; Pred. No. 1.7e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFEEHVAVRANKHLKILNTPCALQIVARLKNNNRQVCIDPKLWIOE 60
 DB 1 KPVSLSTPCPCRFEEHVAVRANKHLKILNTPCALQIVARLKNNNRQVCIDPKLWIOE 60

OY 61 YLEKALN 67

DB 61 YLEKALN 67

RESULT 9
 AAY67594
 ID AAY67594 standard; peptide; 67 AA.

XX AAY67594;

DT 13-JUN-2000 (first entry)

DE SDF-1alpha peptide sequence.

XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;
 KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.

XX Unidentified.

PN WO200009152-A1.

PD 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI: 2000-224175/19.

PT Therapeutic composition containing CXCR4 antagonist, useful for
 PT treating autoimmune disease, especially multiple sclerosis and cancer

XX Disclosure; Fig 1; 88pp; English.

CC The invention provides a therapeutic composition containing an antagonist
 CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions
 CC are specifically used to reduce production of gamma-interferon by T
 CC cells, particularly for treating autoimmune disease, especially multiple
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
 CC colitis, gout, lupus and transplant rejection; to treat cancer by
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
 CC evaluate in vivo pharmacokinetics, or to determine disease progression
 CC and susceptibility, or as targeting agents for delivery of other
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
 CC derived factor one) peptide fragments, SDF-1 being the only known natural
 CC ligand for CXCR4. The present sequence represents a SDF-1alpha
 CC peptide sequence.

XX Sequence 67 AA:

Query Match 95.3%; Score 344; DB 21; Length 67;
 Best Local Similarity 97.0%; Pred. No. 1.7e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFEEHVAVRANKHLKILNTPCALQIVARLKNNNRQVCIDPKLWIOE 60
 DB 1 KPVSLSTPCPCRFEEHVAVRANKHLKILNTPCALQIVARLKNNNRQVCIDPKLWIOE 60

OY 61 YLEKALN 67

RESULT 10
 AAB47680

ID AAB47680 standard; peptide: 67 AA.
 XX
 AC AAB47680;
 XX
 DE 30-JAN-2002 (first entry)
 DT
 XX SDF-1-alpha.
 DE
 XX Haematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Homo sapiens.
 XX
 PN WO200176615-A2.
 PD
 XX 18-OCT-2001.
 PF
 XX 12-APR-2001; 2001WO-CA00540.
 PR
 XX 12-APR-2000; 2000CA-2305036.
 PR 14-SEP-2000; 2000US-232425P.
 PR 23-FEB-2001; 2001CA-2335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
 DR WPI; 2002-025882/03.
 XX
 PT CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation
 PT
 XX
 PS Claim 8: Page 57; 74pp; English.
 XX
 CC The sequences given in AAB47680-717 represent peptides which may be
 CC used in the method of the invention for reducing the rate of
 CC hematopoietic cell multiplication. These peptides act as CXCR4 chemokine
 CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
 CC stromal cell derived factor one (SDF-1) with some also containing
 CC sequences derived from macrophage inflammatory protein 1-alpha
 CC (MIP-1-alpha). They can be used to reduce susceptibility of
 CC hematopoietic cells to a cytotoxic agent, by administering one of the
 CC agonist peptides to the cells prior to or during exposure of the
 CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
 CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
 CC in a patient with cancer requiring autologous or allogenic bone marrow
 CC or peripheral blood stem cell transplantation, or an autoimmune disease.
 CC
 XX
 SQ Sequence 67 AA:
 Query Match 95.3%; Score 344; DB 23; Length 67;
 Best Local Similarity 97.0%; Pred. No. 1.7e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSLSPCCRFPFESHVARANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 ID 1 KPVSLSYRCPCRFPFESHVARANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 1 KPVSLSYRCPCRFPFESHVARANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 QY 61 YLEKALN 67
 ID 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 11
 ID AAM50761 standard; peptide: 68 AA.
 XX
 AC AAM50761;

XX
 DT 27-JUL-1998 (first entry)
 XX
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
 XX
 KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
 XX
 OS Homo sapiens.
 XX
 PN FR2751658-A1.
 PD
 XX 30-JAN-1998.
 PF
 XX 26-JUL-1996; 96FR-0009477.
 PR
 XX 26-JUL-1996; 96FR-0009477.
 XX
 PA (INSP) INST PASTEUR.
 PA Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
 PI WPI; 1998-123039/12.
 DR
 XX
 PT Human stromal cell-derived chemokine, SDF-1 - useful for treating
 PT human immunodeficiency virus infection
 XX
 PS Claim 5; Page 29; 48pp; French.
 XX
 CC The invention relates to peptides which bind to a cellular receptor for
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as Leukocyte-
 CC expressed transmembrane domain receptor), especially where the
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or
 CC prevent HIV infections, optionally together with reverse transcriptase
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-
 CC associated opportunistic infections and/or other CXCR4 or CC chemokines,
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.
 CC
 XX
 SQ Sequence 68 AA:
 Query Match 95.3%; Score 344; DB 19; Length 68;
 Best Local Similarity 97.0%; Pred. No. 1.8e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KGVSLSPCCRFPFESHVARANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 ID 2 KPVSLSYRCPCRFPFESHVARANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61
 DB 2 KPVSLSYRCPCRFPFESHVARANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61
 QY 61 YLEKALN 67
 ID 61 YLEKALN 67
 DB 62 YLEKALN 68
 RESULT 12
 ID AAY05818 standard; Protein: 69 AA.
 XX
 AC AAY05818;
 XX
 DT 02-AUG-1999 (first entry)
 DE
 XX N-terminal modified chemokine met-hsDF-1 alpha.
 DE
 KW Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hsDF-1 alpha;
 KW human; protein engineering; amino-terminal modification; mutant;
 KW HIV; infection; angiogenesis; autoimmune disease; inflammation;
 KW antiangiogenic; antiinflammatory; immunosuppressive; therapy;
 KW vaccine.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX MO9920759-A1.
 PN 29-APR-1999.
 PD 21-OCT-1998; 98WO-US22282.
 XX 20-OCT-1998; 98US-0175713.
 PR 22-OCT-1997; 97US-0955826.
 PR 27-FEB-1998; 98WO-US04002.
 XX (GENY) GENETICS INST INC.
 PA Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
 PI Yang O;
 DR WPI: 1999-288307/24.
 DR N-PSDB: AAX25530.
 XX Modified chemokines useful for inhibiting or stimulating
 PT angiogenesis
 PS Claim 6c: Page 79; 85pp; English.
 XX The present sequence represents met-hsDF-1 alpha, i.e. human
 CC stromal cell derived growth factor-1 alpha having an added
 CC N-terminal methionine residue. DNA encoding met-hsDF-1 alpha (see
 CC AA25530) was produced by cloning an NdeI/XbaI-restricted hSDF-1
 CC alpha PCR product into the E. coli expression vector pAL781
 CC in-frame with an ATG codon. met-hsDF-1 alpha is an example of
 CC novel N-terminal modified chemokines (see AA05818-21) that have at
 CC least one Met residue, at least one aminoxy-pentane residue or at
 CC least one GroHEK peptide (see AA05822) covalently attached at the
 CC N-terminus. The N-terminal modified chemokines are useful for
 CC altering receptor function, inhibiting interactions between
 CC chemokine receptors and their ligands. They are used as research
 CC tools for identifying chemokine receptors, as vaccine adjuvants, as
 CC agents for the chemotactic recruitment of migratory cells, as agents
 CC for the stimulation or inhibition of angiogenesis, as agents against
 CC autoimmune diseases and inflammation, and as agents to inhibit the
 CC binding of HIV to certain receptors and the infection of
 CC susceptible cells by HIV. HIV infection is best treated with
 CC modified SDF-1 alpha and beta or MIP-1 alpha and beta.
 CC
 XX Sequence 69 AA:
 SQ
 Query Match 95.3%; Score 344; DB 20; Length 69;
 Best Local Similarity 97.0%; Pred. No. 1.8e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 2 KPVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61
 OY 61 YLEKALN 67
 DB 62 YLEKALN 68
 RESULT 13
 AAWS0762
 ID AAWS0762 standard; peptide: 72 AA.
 AC AAWS0762;
 XX
 DT 27-JUL-1998 (first entry)
 XX
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.
 XX Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.

XX Homo sapiens.
 OS Synthetic.
 XX FR2751658-A1.
 PN 30-JAN-1998.
 PD 26-JUL-1996; 96FR-0009477.
 XX 26-JUL-1996; 96FR-0009477.
 PR 26-JUL-1996; 96FR-0009477.
 XX (INSP) INST PASTEUR.
 PA Arenzana SE, Baggiolini M, Clark LI, Moser B, Virelizier JL;
 PI WPI: 1998-123039/12.
 DR
 XX Human stromal cell-derived chemokine, SDF-1 - useful for treating
 PT human immunodeficiency virus infection
 PS Claim 5; Page 29; 48pp; French.
 XX The invention relates to peptides which bind to a cellular receptor for
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-
 CC expressed transmembrane domain receptor), especially where the
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or
 CC prevent HIV infections, optionally together with reverse transcriptase
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-
 CC associated opportunistic infections and/or other CXCR4 or CC chemokines,
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be
 CC used to detect anti-SDF-1 antibodies in biological fluids. This
 CC sequence represents a specifically claimed peptide which binds to the
 CC CXCR4 receptor.
 CC
 XX Sequence 72 AA:
 SQ
 Query Match 95.3%; Score 344; DB 19; Length 72;
 Best Local Similarity 97.0%; Pred. No. 1.9e-37;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KGVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 1 KPVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 OY 61 YLEKALN 67
 DB 61 YLEKALN 67
 RESULT 14
 AAY34093
 ID AAY34093 standard; protein: 72 AA.
 AC AAY34093;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Native stromal cell derived factor 1 (SDF-1) beta protein.
 XX
 DE CXCR4 chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KW angiogenesis; stromal cell derived factor 1; SDF-1.
 OS Mammalia.
 XX
 PN WO9947158-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 12-MAR-1999; 99WO-CA00221.
 XX
 PR 13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Clark-Lewis I, Gong J, Duronio V;
XX WPI; 1999-561857/47.
DR
XX
PT Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and
XX cancer -
PS Example 1; Fig 1; 71pp; English.
XX
XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)
CC antagonist for the manufacture of a medicament for reducing interferon
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
CC to treat or to design a medicament to treat, an autoimmune disease, ...
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
CC antagonists may be peptide compounds comprising a substantially purified
CC peptide fragment, analogue or a pharmacologically acceptable salt of
CC stromal cell derived factor 1 (SDF-1). The present sequence represents
CC the amino acid sequence of SDF-1 beta protein.
XX
SQ Sequence 72 AA;
Query Match 95.3%; Score 344; DB 20; Length 72;
Best Local Similarity 97.0%; Pred. No. 1.9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSLSYPCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
DB 61 YLEKALN 67
61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 15
AA67595
ID AA67595 standard; peptide; 72 AA.
XX
AC AA67595;
XX
DT 13-JUN-2000 (first entry)
XX
DE SDF-1beta peptide sequence.
XX
XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.
XX
OS Unidentified.
XX
XX WO200009152-A1.
XX
PD 24-FEB-2000.
XX
PE 16-AUG-1999; 99WO-CA00750.
XX
PR 14-AUG-1998; 98CA-2245224.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Clark-Lewis I, Gong J, Duronio V, Salari H;
XX
DR WPI; 2000-224175/19.
XX
PT Therapeutic composition containing CXCR4 antagonist, useful for
PT treating autoimmune disease, especially multiple sclerosis and cancer
XX

PS Disclosure; Fig 1; 88pp; English.
XX
XX The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells, particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1beta
XX peptide sequence.
XX
SQ Sequence 72 AA;
Query Match 95.3%; Score 344; DB 21; Length 72;
Best Local Similarity 97.0%; Pred. No. 1.9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KGVSLSYPCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLKWIOE 60
DB 61 YLEKALN 67
61 YLEKALN 67
DB 61 YLEKALN 67

Search completed: January 23, 2003, 15:33:43
Job time : 28.2 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:33:47 : Search time 9.8 Seconds
(without alignments)
201.157 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361

Sequence: 1 KGVSLSTPCPCRFESHVAR.....QVCIDPKLKWIDEKALN 67

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents-NA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.3	89	1	US-08-323-084A-1
2	344	95.3	89	1	US-08-674-008-1
3	344	95.3	93	1	US-08-323-084A-5
4	344	95.3	93	1	US-08-674-008-5
5	344	95.3	326	3	US-08-808-720-3
6	344	95.3	328	3	US-08-808-720-1
7	343	95.0	89	1	US-08-181-556-2
8	93.5	25.9	70	1	US-08-330-163-24
9	93.5	25.9	70	1	US-08-482-111-24
10	93.5	25.9	91	2	US-08-633-682-5
11	93.5	25.9	91	3	US-08-936-772-5
12	93.5	25.9	91	4	US-09-395-918-5
13	93.5	25.9	91	4	US-08-679-493A-156
14	91	25.2	71	3	US-08-615-232A-8
15	91	25.2	71	3	US-08-470-323-8
16	90.5	25.1	66	1	US-08-244-702-13
17	90.5	25.1	67	1	US-08-244-702-12
18	90.5	25.1	67	1	US-08-244-702-14
19	90.5	25.1	68	1	US-08-244-702-9
20	90.5	25.1	68	1	US-08-244-702-10
21	90.5	25.1	68	1	US-08-244-702-11
22	90.5	25.1	69	1	US-08-244-702-2
23	90.5	25.1	69	1	US-08-244-702-3
24	90.5	25.1	69	1	US-08-244-702-4
25	90.5	25.1	69	1	US-08-244-702-5
26	90.5	25.1	69	1	US-08-244-702-6
27	90.5	25.1	69	1	US-08-244-702-7

28	90.5	25.1	69	1	US-08-244-702-8	Sequence 8, Appl
29	90.5	25.1	72	1	US-07-956-863-1	Sequence 1, Appl
30	90.5	25.1	72	1	US-07-778-413E-16	Sequence 16, Appl
31	90.5	25.1	72	1	US-08-340-102-16	Sequence 16, Appl
32	90.5	25.1	72	1	US-08-330-163-1	Sequence 1, Appl
33	90.5	25.1	72	1	US-08-330-163-16	Sequence 16, Appl
34	90.5	25.1	72	1	US-08-244-702-1	Sequence 1, Appl
35	90.5	25.1	72	1	US-08-482-111-1	Sequence 1, Appl
36	90.5	25.1	72	1	US-08-482-111-16	Sequence 16, Appl
37	90.5	25.1	72	1	US-08-482-111-47	Sequence 47, Appl
38	90.5	25.1	72	1	US-08-482-111-49	Sequence 49, Appl
39	90.5	25.1	72	1	US-08-202-989-1	Sequence 1, Appl
40	90.5	25.1	72	5	PCR-US94-02051-1	Sequence 1, Appl
41	90.5	25.1	73	1	US-08-482-111-63	Sequence 63, Appl
42	90.5	25.1	73	1	US-08-482-111-65	Sequence 65, Appl
43	90.5	25.1	73	1	US-08-482-111-69	Sequence 69, Appl
44	90.5	25.1	73	1	US-08-482-111-70	Sequence 70, Appl
45	90.5	25.1	73	4	US-09-384-302A-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-323-084A-1
Sequence 1, Application US/08323084A
Patent No. 5563048
GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,084A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-084A-1
Query Match
Best local similarity 95.3%; Score 344; DB 1; Length 89;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLKWIOE 60
Db 22 KPVSLSTPCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67

Matches 20; Conservative 16; Mismatches 21; Indels 3; Gaps 3;
Qy 9 CPCRFFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOEYL 66
Db 10 CLCVKTTSQVRRPHITSLVIAKAGPHCPTAOLIALTK-NGRKLCIDPKENWVKIITKLL 68

RESULT 10

US-08-633-682-5
Sequence 5, Application US/08633682
Patent No. 5840544
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,682
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0063 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 475206
US-08-633-682-5

Query Match 25.9%; Score 93.5; DB 2; Length 91;
Best Local Similarity 34.5%; Pred. No. 4e-05;
Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;
Qy 8 PCCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOEYL 62
Db 32 PCCFAYLSLALPRAHVKY-FYTSSKCSMLAVFVTRRRROYCANPEKKWVOEYI 85

RESULT 11

US-08-936-772-5
Sequence 5, Application US/08936772
Patent No. 6015883
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive

CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,772
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/633,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0063 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 475206
US-08-936-772-5

Query Match 25.9%; Score 93.5; DB 3; Length 91;
Best Local Similarity 34.5%; Pred. No. 4e-05;
Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;

Qy 8 PCCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOEYL 62
Db 32 PCCFAYLSLALPRAHVKY-FYTSSKCSMLAVFVTRRRROYCANPEKKWVOEYI 85

RESULT 12
US-09-395-918-5
Sequence 5, Application US/09395918
Patent No. 6238666
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: DNA ENCODING RANTES HOMOLOG FROM PROSTATE
FILE REFERENCE: PF-0063 US
CURRENT APPLICATION NUMBER: US/09/395,918
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: GenBank: GI 475206
US-09-395-918-5

Query Match 25.9%; Score 93.5; DB 4; Length 91;
Best Local Similarity 34.5%; Pred. No. 4e-05;
Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;
Qy 8 PCCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOEYL 62
Db 32 PCCFAYLSLALPRAHVKY-FYTSSKCSMLAVFVTRRRROYCANPEKKWVOEYI 85

RESULT 13
US-08-679-493A-156
; Sequence 156, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 156
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Mus sp.
US-08-679-493A-156

Query Match
Best Local Similarity 25.9%; Score 93.5; DB 4; Length 91;
Best Local Similarity 34.5%; Pred. No. 4e-05;
Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;

OY 8 PCPCRFESHVARANKHLKILTPNCALQIYARLKNNNROYCIDPKLWIDLEYL 62
DB 32 PCCFAYLSIALRAHKEY-FYTSKSCSNLAVYFTRRRQVCANPEKKWVDYI 85

RESULT 14
US-08-615-232A-8
; Sequence 8, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-615-232A-8

Query Match
Best Local Similarity 25.2%; Score 91; DB 2; Length 71;
Best Local Similarity 29.8%; Pred. No. 6.4e-05;
Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

OY 8 PCPCRFESHVARANKHLKILTPNCALQIYARLKNNNROYCIDPKLWIDLEYL 64
DB 5 PTCCTFFNKQIPLKRVKGYERITSSRCPOEAVIFRTLKNKEVCADPTOKWVDYIAK 61

RESULT 15
US-08-470-323-8
; Sequence 8, Application US/08470323A
; Patent No. 6031080
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/08/470,323A
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: PCT/GB94/02006
; EARLIER FILING DATE: 1994-09-14
; EARLIER APPLICATION NUMBER: GB 9318984.3
; EARLIER FILING DATE: 1993-09-14
; EARLIER APPLICATION NUMBER: GB 94086902.2
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO: 8
; LENGTH: 71
; TYPE: PRT
; ORGANISM: guinea pig
US-08-470-323-8

Query Match
Best Local Similarity 25.2%; Score 91; DB 3; Length 71;
Best Local Similarity 29.8%; Pred. No. 6.4e-05;
Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

OY 8 PCPCRFESHVARANKHLKILTPNCALQIYARLKNNNROYCIDPKLWIDLEYL 64
DB 5 PTCCTFFNKQIPLKRVKGYERITSSRCPOEAVIFRTLKNKEVCADPTOKWVDYIAK 61

Search completed: January 23, 2003, 15:38:59
Job time : 10.8 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 : Search time 6.2 seconds
(without alignments)
218.059 Million cell updates/sec

Title: US-09-852-424-5
361
Sequence: 1 KVSLSYPCPCRFESHVAR.....QVCIDPKIKIQLYKALN 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	100.0	67	9	US-09-852-424-5
2	352	97.5	67	9	US-09-852-424-1
3	352	97.5	67	9	US-09-852-424-9
4	348	96.4	67	9	US-09-852-424-7
5	347	96.1	67	9	US-09-852-424-3
6	347	96.1	67	9	US-09-852-424-6
7	345	95.6	67	9	US-09-852-424-2
8	344	95.3	67	9	US-09-852-424-8
9	344	95.3	67	9	US-09-852-107-1
10	344	95.3	67	10	US-09-144-838-8
11	344	95.3	67	10	US-09-144-838-23
12	344	95.3	89	8	US-08-927-939-22
13	344	95.3	89	9	US-09-792-793A-32
14	344	95.3	89	10	US-09-953-692-4
15	344	95.3	89	10	US-09-953-717-4
16	344	95.3	93	8	US-08-927-939-56
17	344	95.3	93	9	US-09-835-107-2
18	344	95.3	93	9	US-09-835-107-3
19	344	95.3	93	9	US-09-792-793A-93

20	344	95.3	93	10	US-09-144-838-7	Sequence 7, Appl
21	344	95.3	93	10	US-09-919-497-95	Sequence 99, Appl
22	344	95.3	320	9	US-09-792-793A-77	Sequence 77, Appl
23	344	95.3	322	9	US-09-792-793A-78	Sequence 78, Appl
24	344	95.3	327	9	US-09-792-793A-79	Sequence 79, Appl
25	342	94.7	67	9	US-09-852-424-4	Sequence 4, Appl
26	335.5	92.9	66	9	US-09-852-424-12	Sequence 12, Appl
27	333.5	92.4	66	9	US-09-852-424-10	Sequence 10, Appl
28	330.5	91.6	66	9	US-09-852-424-11	Sequence 11, Appl
29	327	90.6	68	10	US-09-144-838-51	Sequence 51, Appl
30	326.5	90.4	66	10	US-09-144-838-27	Sequence 27, Appl
31	309.5	85.7	67	10	US-09-144-838-47	Sequence 47, Appl
32	293	81.2	68	10	US-09-144-838-74	Sequence 24, Appl
33	290	80.3	67	10	US-09-144-838-25	Sequence 25, Appl
34	276	76.5	69	10	US-09-144-838-52	Sequence 52, Appl
35	275.5	76.3	67	10	US-09-144-838-28	Sequence 28, Appl
36	273	75.6	68	10	US-09-144-838-53	Sequence 53, Appl
37	258.5	71.6	68	10	US-09-144-838-48	Sequence 48, Appl
38	255.5	70.8	67	10	US-09-144-838-49	Sequence 49, Appl
39	252.5	69.9	66	10	US-09-144-838-29	Sequence 29, Appl
40	239	66.2	68	10	US-09-144-838-26	Sequence 26, Appl
41	222	61.5	69	10	US-09-144-838-54	Sequence 54, Appl
42	221.5	61.4	67	10	US-09-144-838-50	Sequence 50, Appl
43	221	61.2	67	10	US-09-144-838-31	Sequence 31, Appl
44	210.5	58.3	66	10	US-09-144-838-35	Sequence 35, Appl
45	204.5	56.6	68	10	US-09-144-838-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-852-424-5
Sequence 5, Application US/09852424
Patent No. US20020156034A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia; and
APPLICANT: Chemokine Therapeutics Corporation
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: 80021-257
CURRENT APPLICATION NUMBER: US/09/852,424
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: CA 2,305,787
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 60/205,467
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Engineered in
US-09-852-424-5
OTHER INFORMATION: Laboratory
Query Match
Best Local Similarity 100.0%; Score 361; DB 9; Length 67;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSLSYPCPCRFESHVARAVKHLKITNTPCALQIYARLKNRRVCIDPKLWIOE 60
DB 1 KVSLSYPCPCRFESHVARAVKHLKITNTPCALQIYARLKNRRVCIDPKLWIOE 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67
RESULT 2
US-09-852-424-1
Sequence 1, Application US/09852424

; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; US-09-852-424-1

Query Match 97.5%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 9.7e-33;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYPCGCRFFESHVARANVKKHLKILNTPNCALOIVARLNNNNROVCIDPKLWIOE 60
DB 1 KGVSLSYPCGCRFFESHVARANVKKHLKILNTPNCALOIVARLNNNNROVCIDPKLWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 3
US-09-852-424-9
; Sequence 9, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 67
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; US-09-852-424-9

Query Match 97.5%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 9.7e-33;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYPCGCRFFESHVARANVKKHLKILNTPNCALOIVARLNNNNROVCIDPKLWIOE 60
DB 1 KGVSLSYPCGCRFFESHVARANVKKHLKILNTPNCALOIVARLNNNNROVCIDPKLWIOE 60

OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 4
US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; US-09-852-424-7

Query Match 96.4%; Score 348; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 2.7e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSYPCGCRFFESHVARANVKKHLKILNTPNCALOIVARLNNNNROVCIDPKLWIOE 60
DB 1 KGVSLSYPCGCRFFESHVARANVKKHLKILNTPNCALOIVARLNNNNROVCIDPKLWIOE 60
OY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 5
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory

US-09-852-424-3

Query Match 96.1%; Score 347; DB 9; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.5e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 DB 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 5
 US-09-852-424-6
 ; Sequence 6, Application US/09852424
 ; Patent No. US20020156034A1
 ; GENERAL INFORMATION:

; APPLICANT: The University of British Columbia; and
 ; APPLICANT: Chemokine Therapeutics Corporation

; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
 ; FILE REFERENCE: 80021-257
 ; CURRENT APPLICATION NUMBER: US/09/852,424

; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: CA 2,305,787
 ; PRIOR FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: US 60/205,467

; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6

; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; NAME/KEY: MUTAGEN

; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
 ; OTHER INFORMATION: disclosure for possible structures for P*
 ; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
 ; OTHER INFORMATION: Laboratory
 US-09-852-424-6

Query Match 96.1%; Score 347; DB 9; Length 67;
 Best Local Similarity 97.0%; Pred. No. 3.5e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 DB 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 7
 US-09-852-424-2
 ; Sequence 2, Application US/09852424
 ; Patent No. US20020156034A1
 ; GENERAL INFORMATION:

; APPLICANT: The University of British Columbia; and
 ; APPLICANT: Chemokine Therapeutics Corporation

; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
 ; FILE REFERENCE: 80021-257
 ; CURRENT APPLICATION NUMBER: US/09/852,424

; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: CA 2,305,787
 ; PRIOR FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: US 60/205,467
 ; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2

; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
 ; OTHER INFORMATION: Laboratory
 US-09-852-424-2

Query Match 95.6%; Score 345; DB 9; Length 67;
 Best Local Similarity 97.0%; Pred. No. 5.8e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 DB 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 8
 US-09-852-424-8
 ; Sequence 8, Application US/09852424
 ; Patent No. US20020156034A1
 ; GENERAL INFORMATION:

; APPLICANT: The University of British Columbia; and
 ; APPLICANT: Chemokine Therapeutics Corporation

; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
 ; FILE REFERENCE: 80021-257
 ; CURRENT APPLICATION NUMBER: US/09/852,424

; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: CA 2,305,787
 ; PRIOR FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: US 60/205,467

; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8

; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; NAME/KEY: MUTAGEN

; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
 ; OTHER INFORMATION: disclosure for possible structures for P*
 ; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
 ; OTHER INFORMATION: Laboratory
 US-09-852-424-8

Query Match 95.3%; Score 344; DB 9; Length 67;
 Best Local Similarity 97.0%; Pred. No. 7.5e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60
 DB 1 KGVSLSPGCRPFREFSHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60

OY 61 YLEKALN 67
 DB 61 YLEKALN 67

RESULT 9
 US-09-835-107-1
 ; Sequence 1, Application US/09835107
 ; Patent No. US20020165123A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tudan, Christopher R.

APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Castman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: SDF-1 alpha
US-09-835-107-1

Query Match 95.3%; Score 344; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 7.5e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60
DB 1 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 10
US-09-144-838-8
Sequence 8, Application US/09144838A
Patent No. US20020051996A1
GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GRN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8

Query Match 95.3%; Score 344; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 7.5e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60
DB 1 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60

QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 11
US-09-144-838-23
Sequence 23, Application US/09144838A
Patent No. US20020051996A1
GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GRN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-23

Query Match 95.3%; Score 344; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 7.5e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60
DB 1 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60
QY 61 YLEKALN 67
DB 61 YLEKALN 67

RESULT 12
US-08-927-939-22
Sequence 22, Application US/08927939
Patent No. US20010006640A1
GENERAL INFORMATION:
APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauren Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022US1
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
US-08-927-939-22

Query Match 95.3%; Score 344; DB 8; Length 89;
Best Local Similarity 97.0%; Pred. No. 9.9e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 60
DB 22 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLNNNNQVCIDPKLWIOE 81
QY 61 YLEKALN 67

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds
(without alignments)
555.259 Million cell updates/sec

Title: US-09-852-424-5
Perfect score: 361
Sequence: 1 KGVSLSYPCPCRFESHVAR.....QVCIDPKLKMIGVLEKALN 67

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.3	93	2	G01540
2	343	95.0	89	2	A53497
3	343	95.0	89	2	I53416
4	343	95.0	93	2	I81182
5	98	27.1	101	2	I48148
6	93.5	25.9	91	1	A46539
7	91	25.2	95	2	JN0841
8	91	25.2	120	2	I48147
9	90.5	25.1	99	2	A37034
10	88.5	24.5	91	1	A28815
11	87	24.1	101	2	I42496
12	86.5	24.0	96	2	A32954
13	85	23.5	103	2	A53096
14	85	23.5	109	2	A54678
15	84.5	23.4	870	2	A41130
16	84	23.3	101	2	I46871
17	82.5	22.9	96	2	JN0572
18	81.5	22.6	92	2	I52322
19	81	22.4	120	2	JEO177
20	81	22.4	148	1	A30209
21	81	22.4	148	1	S07723
22	78.5	21.7	100	2	JH0200
23	77.5	21.5	75	2	A54188
24	76.5	21.2	75	2	B54188
25	76.5	21.2	119	2	S42881
26	76	21.1	96	2	I48099
27	75.5	20.9	107	2	B38290
28	73.5	20.4	92	2	I46730
29	73.5	20.4	96	2	JC3478

30	73.5	20.4	100	2	S21467	macrophage inflamm
31	73.5	20.4	100	2	I55614	macrophage inflamm
32	73.5	20.4	103	2	A26736	transformation-ind
33	73.5	20.4	103	2	I50417	RSV-induced protei
34	73.5	20.4	132	2	A57325	C-X-C chemokine Li
35	72.5	20.1	101	2	B28414	growth-regulated p
36	72.5	20.1	107	2	A28414	melanoma growth-st
37	72.5	20.1	114	2	A55010	neutrophil-activat
38	72.5	20.1	117	2	B44253	alveolar macrophag
39	72	19.9	92	2	A32393	macrophage inflamm
40	70.5	19.5	53	2	I64831	gene KC protein -
41	69.5	19.3	622	2	A45255	Dp71 protein - hum
42	69.5	19.3	3678	2	S28916	dystrophin - mouse
43	69.5	19.3	3685	1	A27605	dystrophin, muscle
44	69	19.1	93	2	B35673	platelet factor 4
45	68.5	19.0	104	1	PH04A	platelet factor 4

ALIGNMENTS

RESULT 1
G01540
cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C:Accession: G01540
R:Spolilla, L.D.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07697
A:Accession: G01540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <SPO>
A:Cross-references: EMBL:U16752; NID:q1272194; PID:9571508
C:Superfamily: beta-thromboglobulin

Query Match 95.3% Score 344; DB 2; Length 93;
Best Local Similarity 97.0%; Pred. No. 1,le-34;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	KGVSLSYPCPCRFESHVARAVKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60	
DB	22	KPVSLSYPCPCRFESHVARAVKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 81	
QY	61	YLEKALN 67	
DB	82	YLEKALN 88	
RESULT 2			
A53497			
pre-B-cell growth-stimulating factor precursor - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000			
C:Accession: A53497; I59582			
R:Nagasawa, T.; Kikutan, H.; Kishimoto, T.			
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994			
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.			
A:Reference number: A53497; MUID:94181581; PMID:8134392			
A:Accession: A53497			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-89 <NAG>			
A:Cross-references: GB:D21072; NID:9413905; PID:BA04648.1; PID:9468457			
R:Tashiro, K.; Tada, H.; Heliker, R.; Shirozu, M.; Nakano, T.; Honjo, T.			
Science 261, 600-603, 1993			
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me			
A:Reference number: I59582; MUID:93342488; PMID:8342023			
A:Accession: I59582			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-89 <RES>			

A:Cross-references: GB:LI2029; NID:g393179; PIDN:AAA40100.1; PID:g393180
 C:Genetics:
 A:Gene: SDF-1-alpha
 C:Superfamily: beta-thromboglobulin
 C:Keywords: cytokine

Query Match 95.0%; Score 343; DB 2; Length 89;
 Best Local Similarity 95.5%; Pred. No. 1.4e-34;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSTPCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 22 KPVSLSTRCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 3

I33416
 Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 05-Nov-1999
 C:Accession: I33416
 R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
 Exp. Cell Res. 215, 284-293, 1994
 A:Title: Molecular cloning of TPRL, a gene whose expression is repressed by the tumor F
 A:Reference number: I33416; MUID:95073497; PMID:7982471

A:Accession: I33416
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-89 <RES>

A:Cross-references: GB:S7418; NID:g786393; PIDN:AA32650.1; PID:g786394
 C:Genetics:
 A:Gene: TPRL
 C:Superfamily: beta-thromboglobulin

Query Match 95.0%; Score 343; DB 2; Length 89;
 Best Local Similarity 95.5%; Pred. No. 1.4e-34;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSTPCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 22 KPVSLSTRCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 4

I81182
 Cytokine - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 05-Nov-1999
 C:Accession: I81182
 R:Tashiro, K.; Tada, H.; Heiker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
 Science 261, 600-603, 1993
 A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr
 A:Reference number: I59582; MUID:93342488; PMID:8342023
 A:Accession: I81182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-93 <RES>
 A:Cross-references: GB:LI2030; NID:g393181; PIDN:AAA40101.1; PID:g393182
 C:Genetics:
 A:Gene: SDF-1-beta
 C:Superfamily: beta-thromboglobulin

Query Match 95.0%; Score 343; DB 2; Length 93;
 Best Local Similarity 95.5%; Pred. No. 1.4e-34;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSTPCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
 DB 22 KPVSLSTRCRCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
 QY 61 YLEKALN 67
 DB 82 YLEKALN 88

RESULT 5

I48148
 Neutrophil attractant protein-1 - guinea pig

C:Species: Cavia porcellus (guinea pig)
 C:Date: 02-Jul-1996 #sequence-revision 02-Jul-1996 #text-change 20-Aug-1999
 C:Accession: I48148
 R:Toshimura, T.; Johnson, D.G.
 J. Immunol. 151, 6225-6236, 1993
 A:Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (N
 A:Reference number: I48148; MUID:94065176; PMID:7504015
 A:Accession: I48148
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-101 <RES>
 A:Cross-references: GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765
 C:Genetics:
 A:Gene: NAP-1
 C:Superfamily: beta-thromboglobulin

Query Match 27.1%; Score 98; DB 2; Length 101;
 Best Local Similarity 34.4%; Pred. No. 9.9e-05;
 Matches 21; Conservative 17; Mismatches 17; Indels 6; Gaps 4;

QY 11 CRFEESHVARAN--VKHKLKILNTPNCA-LQIVARLKNNNRQVCIDPKLKWIOE 65
 DB 34 CQCITKIHHTTPHPPFKTELKVESGPCANSEITVRL-SDNRQLCIDPKKRWQDVVSMF 92

QY 66 L 66
 DB 93 L 93

RESULT 6

A46539
 monocyte chemoattractant cytokine RANTES precursor - mouse

N:Alternate names: Muranates
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Jun-1993 #sequence-revision 16-Aug-1996 #text-change 22-Jun-1999
 C:Accession: I48875; A46539; I48654; I36970
 R:Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.
 J. Immunol. 152, 1182-1189, 1994
 A:Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gen
 A:Reference number: I48875; MUID:94132613; PMID:7507961
 A:Accession: I48875
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-91 <DAN>
 A:Cross-references: EMBL:U02298; NID:g460090; PIDN:AAA13302.1; PID:g460091
 R:Schell, T.J.; Simpson, N.J.; Mak, J.Y.
 Eur. J. Immunol. 22, 1477-1481, 1992
 A:Title: Molecular cloning and expression of the murine RANTES cytokine: structural a
 A:Reference number: A46539; MUID:92289805; PMID:1376260
 A:Accession: A46539

A:Molecule type: mRNA
 A:Residues: 1-18, 'A', '20-91 <SCH>
 A:Cross-references: GB:S37648; NID:g250207; PIDN:AA822330.1; PID:g250208
 A:Experimental source: macrophage cell line P05-1.8

A:Note: sequence extracted from NCBI backbone (NCBIN:106768, NCBIP:106770)
 R:Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.
 Mol. Cell. Biol. 14, 2914-2925, 1994

A:Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking reg
 A:Reference number: I48654; MUID:94217689; PMID:7513046
 A:Accession: I48654

A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-91 <SH1>
 A:Cross-references: EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206
 R:Neilson, E.G.; Krensky, A.
 A:Title: Isolation and characterization of cDNA from renal tubular epithelium encoding p
 A:Reference number: 156970; MUID:92277990; PMID:1375672
 A:Accession: 156970
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-40, 'E', 42-91 <NE1>
 A:Cross-references: GB:M77747; NID:g200649; PIDN:AAA40029.1; PID:g200650
 C:Comment: This chemottractant for monocytes but not neutrophils is an immediate-early
 C:Genetics:
 A:Introns: 26/1: 63/2
 C:Superfamily: macrophage inflammatory protein
 C:Keywords: chemokines; cytokine; immediate-early protein; inflammation
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-91/Product: monocyte chemottractant cytokine RANTES #status predicted <MAT>
 Query Match 25.9%; Score 93.5; DB 1; Length 91;
 Best Local Similarity 34.5%; Pred. No. 0.00031;
 Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;
 Oy 8 PCPCFFESHVARANVKKILINPNCALQIVARLKNNNROYCIDPKLWIOEYL 62
 Db 32 PCCFAYLSALPRAHVKY-FTTSSKCSMLAVFVTRRNOVCANPEKMWQVEYI 85
 RESULT 7
 JN0841
 Interleukin-8 - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995
 C:Accession: JN0841
 R:ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
 Gene 131, 305-306, 1993
 A:Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene.
 A:Reference number: JN0841; MUID:94010328; PMID:7916715
 A:Accession: JN0841
 A:Molecule type: DNA
 A:Residues: 1-95 <ISH>
 C:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is inv
 C:Genetics:
 A:Introns: 22/1: 67/2
 C:Superfamily: beta-thromboglobulin
 Query Match 25.2%; Score 91; DB 2; Length 95;
 Best Local Similarity 33.3%; Pred. No. 0.00066;
 Matches 22; Conservative 15; Mismatches 21; Indels 8; Gaps 4;
 Oy 3 VLSLPCPCFFESHVARANVKKILINT---PNCA-LQIVARLKNNNROYCIDPKLW 57
 Db 28 VSELRCOC-IKTSTFPHPKYIKELRYDGPCHENSEIIVKLFNGN-EVCLDPKEKW 84
 Oy 58 IOEYLE 63
 Db 85 VQKVVO 90
 RESULT 8
 I48147
 monocyte chemottractant protein-1 - guinea pig
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I48147
 R:Yoshimura, T.
 J. Immunol. 150, 5025-5032, 1993
 A:Title: cDNA cloning of guinea pig monocyte chemottractant protein-1 and expression of
 A:Reference number: I48147; MUID:93267104; PMID:8496603
 A:Accession: I48147
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-120 <RES>
 A:Cross-references: GB:I04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
 C:Genetics:
 A:Superfamily: macrophage inflammatory protein
 C:Gene: MCP-1
 Query Match 25.2%; Score 91; DB 2; Length 120;
 Best Local Similarity 29.8%; Pred. No. 0.00085;
 Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;
 Oy 8 PCPCFFESHVARANVKKILINPNCALQIVARLKNNNROYCIDPKLWIOEYLEK 64
 Db 31 PCCTCFNNQIDLKRKKYGERITSSRCPEQAVIFRLTKKEVCADPTQKMWQDIYAK 87
 RESULT 9
 A37034
 Interleukin-8 precursor - human
 N:Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-a
 te-derived neutrophil chemotactic factor; monocyte-derived neutrophil-activating fact
 C:Species: Homo sapiens (man)
 C:Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 20-Aug-1999
 C:Accession: A37034; JI0041; A37791; S37634; P10107; A28598; A27488; A39960; A60401;
 R:Mukaida, N.; Shiroo, M.; Matsushima, K.
 J. Immunol. 143, 1366-1371, 1989
 A:Title: Genomic structure of the human monocyte-derived neutrophil chemotactic facto
 A:Reference number: A37034; MUID:89309826; PMID:2653993
 A:Accession: A37034
 A:Molecule type: DNA
 A:Residues: 1-99 <MUK>
 A:Cross-references: GB:M28130; NID:g186367; PIDN:AAA59158.1; PID:g186368
 A:Note: the authors failed to translate the last thirty-six nucleotides of the second
 R:Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavu, S.; Kobayashi, Y.; Lew, W.; App
 J. Exp. Med. 167, 1883-1893, 1988
 A:Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor
 A:Reference number: JI0041; MUID:88258376; PMID:3260265
 A:Accession: JI0041
 A:Molecule type: mRNA
 A:Residues: 1-99 <MAL>
 A:Cross-references: EMBL:Y00787; NID:g34518; PIDN:CAA68742.1; PID:g34519
 A:Note: the sequence shows similarity to several platelet-derived factors, a v-src-in
 R:Kowalski, J.; Denhardt, D.T.
 Mol. Cell. Biol. 9, 1946-1957, 1989
 A:Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in
 A:Reference number: A3791; MUID:89313739; PMID:2664463
 A:Accession: A3791
 A:Molecule type: mRNA
 A:Residues: 1-99 <KOW>
 A:Cross-references: GB:M26383; NID:g188627; PIDN:CAA36323.1; PID:g188628
 R:King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedot, J.R.
 submitted to the EMBL Data Library, February 1992
 A:Reference number: S37634
 A:Accession: S37634
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-97 <KIN>
 A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
 R:Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno,
 J. Exp. Med. 169, 1895-1901, 1989
 A:Title: Purification and partial primary sequence of a chemotactic protein for polym
 A:Reference number: P10107; MUID:89279141; PMID:2659722
 A:Accession: P10107
 A:Molecule type: Protein
 A:Residues: 23-32, 'X', '35', 'X', '37-52', 'V', '54 <SU2>
 A:Experimental source: lung giant cell carcinoma LUG5C
 R:Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.
 Biochem. Biophys. Res. Commun. 151, 883-890, 1988
 A:Title: Structure determination of a human lymphocyte derived neutrophil activating
 A:Reference number: A28598; MUID:88162914; PMID:3279957
 A:Accession: A28598
 A:Molecule type: Protein
 A:Residues: 28-99 <GRD>

R.Waltz, A.; Peveril, P.; Aschauer, H.; Baggiolini, M.
Biochem. Biophys. Res. Commun. 149, 755-761, 1987
A>Title: Purification and amino acid sequencing of NAF, a novel neutrophil-activating factor
A:Reference number: A27468; MUID:88106502; PMID:332281
A:Accession: A27468
A:Molecule type: protein
A:Residues: 28-59 <MAL>
R.Yoshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987
A>Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has
A:Reference number: A39960; MUID:88097462; PMID:3480540
A:Accession: A39960
A:Molecule type: protein
A:Residues: 28-69 <YOS>
R.Schoeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
J. Immunol. 144, 2223-2232, 1990
A>Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8
A:Reference number: A60401; MUID:90187866; PMID:2179408
A:Accession: A60401
A:Molecule type: protein
A:Residues: 23-32 <SCH>
A:Experimental source: dermal fibroblasts
A:Note: a minor component of this material (15%) includes an additional two amino acids
R.Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenacker, G.; Billiau, A.
Eur. J. Immunol. 19, 1189-1194, 1989
A>Title: The chemotactic activity for granulocytes produced by virally infected fibroblasts
A:Reference number: A60591; MUID:89338542; PMID:2668011
A:Accession: A60591
A:Molecule type: protein
A:Residues: 23-33, 'X', '35', 'X', '37-42 <VAN>
R.Nakagawa, H.; Hatakeyama, S.; Ikeue, A.; Miyai, H.
FEBS Lett. 282, 412-414, 1991
A>Title: Generation of Interleukin-8 by plasmin from AVLPR-interleukin-8, the human fibrinolytic
A:Reference number: S15827; MUID:91243843; PMID:1828038
A:Accession: S15827
A:Molecule type: protein
A:Residues: 23-33, 'X', '35', 'X', '37-47 <FEB>
R.Van Damme, J.; Van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.
Eur. J. Biochem. 181, 337-344, 1989
A>Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-terminal
A:Reference number: S04216; MUID:89231715; PMID:2523801
A:Accession: S04216
A:Molecule type: protein
A:Residues: 21-67 <VA2>
R.Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, A.
Mol. Immunol. 26, 87-93, 1989
A>Title: Three forms of monocyte-derived neutrophil chemotactic factor (MNCF) distinguish
A:Reference number: A60567; MUID:89181632; PMID:2648135
A:Accession: A60567
A:Molecule type: protein
A:Residues: 21-33, 'X', '35', 'X', '37-47 <Y02>
A:Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%,
R.Van Damme, J.; Van Beeumen, J.; Opdenacker, G.; Billiau, A.
J. Exp. Med. 167, 1364-1376, 1988
A>Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neutrophil
A:Reference number: A60847; MUID:88187604; PMID:3258625
A:Accession: A60847
A:Molecule type: protein
A:Residues: 28-47 <VA3>
R.Car, B.D.; Baggiolini, M.; Waltz, A.
Biochem. J. 275, 581-584, 1991
A>Title: Formation of neutrophil-activating peptide 2 from platelet-derived connective-tissue
A:Reference number: S15417; MUID:91248085; PMID:2039437
A:Accession: S15417
A>Status: preliminary
A:Molecule type: protein
A:Residues: 28-99 <CAR>
R.Golds, E.E.; Mason, P.; Mylirkos, P.
Biochem. J. 259, 585-588, 1989
A>Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neutrophil-activating factor
A:Reference number: S03975; MUID:89246368; PMID:2655583
A:Accession: S03975
A:Molecule type: protein

A:Residues: 23-46 <GO>
R.Hotta, K.; Hayashi, R.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizuno, S.; Suzuki
Immunol. Lett. 24, 165-170, 1990
A>Title: Coding region structure of Interleukin-8 gene of human lung giant cell carcinoma
A:Reference number: I54560; MUID:90346419; PMID:12200751
A:Accession: I54560
A>Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-99 <RES>
A:Cross-references: GB:D14283; NID:g219915; PIDN:BAA03245.1; PID:g219916
J.Schmid, J.; Weismann, C.
J.Immunol. 139, 250-256, 1987
A>Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like protein
A:Reference number: I55992; MUID:87224164; PMID:2953813
A:Accession: I55992
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-99 <RE2>
A:Cross-references: GB:M17017; NID:g179579; PIDN:AAA3611.1; PID:g179580
R.Kusner, D.J.; Luebers, E.L.; Nowinski, R.J.; Kondraskowski, M.; Kling, G.H.; Sedot,
Kidney Int. 39, 1240-1248, 1991
A>Title: Cyclokin- and IPS-induced synthesis of interleukin-8 from human mesangial cells
A:Reference number: I37902; MUID:91374977; PMID:1895676
A:Accession: I37902
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-97 <RE3>
A:Cross-references: EMBL:Z11686; NID:933958; PIDN:CAA77745.1; PID:g33959
R.Alouani, S.; Gaerther, H.F.; Memrod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.;
Eur. J. Biochem. 227, 328-334, 1995
A>Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling a
A:Reference number: S67519; MUID:95154308; PMID:7851404
A:Accession: S67519
A:Molecule type: mRNA
A:Residues: 1-99 <ALO>
C.Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
C:Comment: This protein is variably processed at the amino end. The major form differ
C:Genetics:
A:Gene: GDB:IL8
A:Cross-references: GDB:I20099; OMIM:146930
A:Map position: 4q13-q21
A:Introns: 22/1; 67/2; 95/2
C:Superfamily: beta-chromoglobin
C:Keywords: chemotaxis; cytokine; inflammation
F.1-20/Domains: signal sequence #status predicted <SIG>
F.1-99/Product: interleukin-8, minor form #status experimental <MATAS>
F.23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <M
F.28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experi

	Query Match	Best Local Similarity	Conservative	Mismatches	Indels	Gaps
OY	23 VKHKLNT-PNCA-LQTVARKNNROVCI	25.1%; Score 90.5;	Pred. No. 0.0008;	Matches 17;	Conservative 16;	Mismatches 10;
DG	49 IKELRVIESGHPCANTEITIVKL-SDGRC	Length 99;	DB 2;	Indels 3;	Gaps 3;	

RESULT 10
A28815
monocyte chemoattractant cytokine RANTES precursor - human
N:Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 16-Aug-1996 #text_change 29-May-1998
C:Accession: A28815
R.Schall, T.J.; Jongstra, J.; DYER, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;
J.Immunol. 141, 1018-1025, 1988
A>Title: A human T cell-specific molecule is a member of a new gene family.
A:Reference number: A28815; MUID:88285659; PMID:2456337
A:Accession: A28815
A:Molecule type: mRNA
A:Residues: 1-91 <SCH>
A:Cross-references: GB:M21121

C:Comment: The acronym RANTES reflects the description "Regulated upon Activation, Normal C:Genetics:
A:Gene: GDB:SCYA5: D17S136E
A:Cross-references: GDB:120749; OMIM:187011
A:Map position: 1/q11.2-17q12
C:Superfamily: macrophage inflammatory protein
C:Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 24.5%; Score 88.5; DB 1; Length 91;
Best Local Similarity 30.9%; Pred. No. 0.0033;
Matches 17; Conservative 12; Mismatches 25; Indels 1; Gaps 1;

OY 8 PCPCRFESHVARANKHLKILNTPNCA-LQIYARLKNNNROYCIDPKLKWIDLEYL 62
DB 32 PCCFATIAIRLPRAHRIKEY-FYTSGRKSNPAAVFVTRKNROYCANPEKKWREYI 85

RESULT 11
SA2496
Interleukin-8 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-Jan-2001
C:Accession: SA2496; 146997
R:Legestols, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.
submitted to the EMBL Data Library, March 1994
A:Description: Nucleotide sequence of ovine Interleukin 8 cDNA using polymerase chain re
A:Reference number: SA2496
A:Accession: SA2496
A:Molecule type: mRNA
A:Residues: 1-101 <LEG>
A:Cross-references: EMBL:X78306; NID:9463253; PIDN:CAA55115.1; PID:9463254
R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine Inte
A:Reference number: 146997; MUID:95137691; PMID:835984
A:Accession: 146997
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-101 <SEO>
A:Cross-references: GB:S74436; NID:9786590; PIDN:AA833241.1; PID:9786591
C:Genetics:
A:Gene: IL-8
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-101/Product: Interleukin-8 #status predicted <MAT>

Query Match 24.1%; Score 87; DB 2; Length 101;
Best Local Similarity 29.5%; Pred. No. 0.0022;
Matches 18; Conservative 20; Mismatches 17; Indels 6; Gaps 4;

OY 11 CFFFSHVVARAN---VKHLKITLNT-PNCA-LQIYARLKNNNROYCIDPKLKWIDLEYL 65
DB 34 CCQITHSTPRHPKFIKELRVIESGPHCENSEIYKLV-NGKEVCLDPKKNVQKVVQAF 92

OY 66 L 66
DB 93 L 93

RESULT 12
A32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating ac
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1999 #text_change 20-Aug-1999
C:Accession: A32954; JH0081
R:Quendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protei
A:Reference number: A32954; MUID:89139485; PMID:2917992

A:Accession: A32954
A:Molecule type: mRNA
A:Residues: 1-96 <QOU>
A:Cross-references: GB:J04596; NID:9201042; PIDN:AAA40131.1; PID:9201043
R:Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou
A:Reference number: JH0081; MUID:89078502; PMID:2909392
A:Accession: JH0081
A:Molecule type: mRNA
A:Residues: 1-96 <RYS>
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C:Genetics:
A:Map position: 5
C:Superfamily: beta-thromboglobulin
C:Keywords: extracellular protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-96/Product: gro-alpha #status predicted <MAT>

Query Match 24.0%; Score 86.5; DB 2; Length 96;
Best Local Similarity 31.7%; Pred. No. 0.0024;
Matches 19; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

OY 9 PCPCRFESHVARANKHLKIL-NTNCA-LQIYARLKNNNROYCIDPKLKWIDLEYL 66
DB 33 CCCLQTMAGIHLKNIOSLVLPSGPHCTQTEVATLTK-NGREACLDPEAPLVQKIVQKML 91

RESULT 13
A53096
Interleukin-8 precursor - pig
N:Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Jan-2001
C:Accession: A53096; A44253
R:Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta
J. Biol. Chem. 269, 77-85, 1994
A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba
A:Reference number: A53096; MUID:94103307; PMID:8276881
A:Accession: A53096
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <LIN>
A:Cross-references: GB:M69923; NID:9164520; PIDN:AAAL6616.1; PID:9164521
R:Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kulper, J.L.; Forstrom,
Biochemistry 31, 10483-10490, 1992
A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotac
A:Reference number: A44253; MUID:93041741; PMID:1420165
A:Accession: A44253
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-22, 'D', 24-103 <GOO>
A:Cross-references: GB:M9367; NID:91235611
A:Experimental source: alveolar macrophage
A>Note: sequence extracted from NCBI backbone (NCBIN:117415, NCBIPI:117416)
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-103/Product: Interleukin-8 #status predicted <MAT>

Query Match 23.5%; Score 85; DB 2; Length 103;
Best Local Similarity 30.3%; Pred. No. 0.0039;
Matches 20; Conservative 18; Mismatches 20; Indels 8; Gaps 5;

OY 3 VLSLPCPCRFESHVARAN---VKHLKITLNT-PNCA-LQIYARLKNNNROYCIDPKLKW 57
DB 28 VSAELRCQC--INTHSTPRHPKFIKELRVIESGPHCENSEIYKLV-NGKEVCLDPKKNW 84

OY 58 IOEYLE 63
DB 85 VQKVVQ 90

RESULT 14

A54678

monocyte chemotactic protein 3 precursor - human

N:Alternate names: monocyte chemoattractant protein MCP-3

C:Species: Homo sapiens (man)

C:Date: 28-Oct-1994 #sequence, revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A54678; JCI478; S32222

R:Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.

Genomics 21, 403-408, 1994

A:Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the

A:Reference number: A54678; MIM:94375065; PMID:7916328

A:Accession: A54678

A:Molecule type: DNA

A:Residues: 1-109 <OPD>

A:Cross-references: GB:X72309

R:Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J..

Biochem. Biophys. Res. Commun. 191, 535-542, 1993

A:Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and

A:Reference number: JCI478; MIM:93213290; PMID:8461011

A:Accession: JCI478

A:Molecule type: mRNA

A:Residues: 1-109 <OP2>

A:Cross-references: GB:X72308; GB:S57464; NID:93928270; PIDN:CA51055.1; PID:9313708

R:Miny, A.; Chalon, P.; Guillemet, J.C.; Kagnad, M.; Lauzun, P.; Magazin, M.; Miloux,

submitted to the EMBL Data Library, March 1993

A:Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoatrac

A:Reference number: S32222

A:Accession: S32222

A:Molecule type: mRNA

A:Residues: 1-109 <MIN>

A:Cross-references: EMBL:X71087; NID:9288396; PIDN:CA50405.1; PID:9288397

C:Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m

C:Genetics:

A:Gene: GDB:SCYA7; SCYA6; MCP-3

A:Cross-references: GDB:138473; OMIM:158106

A:Map position: 17q11-17q12

A:Introns: 36/1; 75/2

A:Superfamily: macrophage inflammatory protein

C:Keywords: cytokine; glycoprotein; inflammation

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>

F:39/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 23.5%; Score 85; DB 2; Length 109;

Matches 13; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 2 GVSLSYPCPCRFESHVARANVHKLILNTPNCALQIVARLKNNRQVCIDPKLKIQEX 61

DB 37 GINTSTCCYRFINKKIPKORLESYRRTSSHCPRAVIFKTKLDKICADPTQKNVQDF 96

QY 62 LE 63

DB 97 MK 98

RESULT 15

A41130

dystrophin homolog - Pacific electric ray (fragment)

N:Alternate names: 300K subynaptic protein

C:Species: Torpedo californica (Pacific electric ray)

C:Date: 03-Aug-1992 #sequence, revision 03-Aug-1992 #text_change 16-Jul-1999

C:Accession: A41130

R:Yeaton, J.E.; Lin, H.; Dyer, S.M.; Burden, S.J.

J. Cell Biol. 115, 1069-1076, 1991

A:Title: Dystrophin is a component of the subynaptic membrane.

A:Reference number: A41130; MIM:92064638; PMID:1720119

A:Accession: A41130

A:Molecule type: mRNA

A:Residues: 1-870 <VEA>

A:Cross-references: GB:M37645

C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrop

F:2-129/Domain: spectrin/dystrophin repeat homology <SP1>
 F:131-238/Domain: spectrin/dystrophin repeat homology <SP2>
 F:253-290/Domain: WW repeat homology <WW1>

Query Match

Best Local Similarity 23.4%; Score 84.5; DB 2; Length 870;

Matches 20; Conservative 7; Mismatches 27; Indels 5; Gaps 1;

QY 5 LSYPCPCRFESHVARANVHKLILNTPNCALQIVARLKN-----NRQVCIDPKLKI 58

DB 322 LSLPSCAEAFDQHNKQNDQLDILEITINCLTSYDRLEQESHNVVPLCYDMCLNWL 380

Search completed: January 23, 2003, 15:37:25
 Job time : 11.6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 : Search time 6 Seconds

(without alignments)
463.152 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361

Sequence: 1 KGVSLSYPCPCRFESHVAR.....QVCIDPKLKIQIYELKALN 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	344	95.3	93	1 SDF1_FELCA	062657 felis silve
2	344	95.3	93	1 SDF1_HUMAN	P48061 homo sapien
3	343	95.0	89	1 SDF1_MOUSE	P40224 mus musculu
4	98	27.1	101	1 IL8_CAVPO	P49113 cavia porce
5	94	26.0	101	1 IL8_CANFA	P41324 canis famill
6	93.5	25.9	91	1 SY05_MOUSE	P30882 mus musculu
7	93.5	25.9	92	1 SY05_RAT	P50231 rattus norv
8	91	25.2	101	1 IL8_FELCA	Q98455 felis silve
9	91	25.2	120	1 SY02_CAVPO	O08782 cavia porce
10	90.5	25.1	99	1 IL8_HUMAN	P10145 h interleuk
11	88.5	24.5	91	1 SY05_HUMAN	P13501 homo sapien
12	87.5	24.2	91	1 SY05_CAVPO	P97272 cavia porce
13	87.5	24.1	101	1 IL8_MCMU	P51495 macaca mula
14	87	24.2	101	1 IL8_SHEEP	P36925 ovls aries
15	86.5	24.0	96	1 GRO_MOUSE	P12850 mus musculu
16	85.5	23.7	101	1 IL8_CERTO	P46653 cercocebus
17	85	23.5	99	1 SY07_HUMAN	P80098 homo sapien
18	85	23.5	103	1 IL8_PIG	P26894 sus scrofa
19	84.5	23.4	98	1 SY13_HUMAN	Q99616 homo sapien
20	84	23.3	101	1 IL8_BOVIN	P19255 bos taurus
21	84	23.3	101	1 IL8_RABIT	P19874 coryctolagus
22	83.5	23.1	91	1 SY05_BOVIN	O97019 bos taurus
23	83	23.0	97	1 SY08_MOUSE	O92121 mus musculu
24	83	23.0	130	1 SY05_RAT	P97885 rattus norv
25	82.5	22.9	96	1 GRO_RAT	P14095 rattus norv
26	82	22.9	50	1 SY05_PIG	Q29288 sus scrofa
27	81.5	22.6	92	1 SY03_RAT	P50229 rattus norv
28	81	22.4	148	1 SY02_MOUSE	P10148 mus musculu
29	81	22.4	148	1 SY02_RAT	P14844 rattus norv
30	80	22.2	120	1 SY16_HUMAN	O13467 h small ind
31	79	21.9	89	1 SY18_HUMAN	P55774 h small ind
32	78.5	21.7	100	1 MIP2_MOUSE	P10889 mus musculu
33	78	21.6	119	1 SY24_MOUSE	O9jkc0 mus musculu

34	77.5	21.5	97	1 E07A_MOUSE	P48298 mus musculu
35	77.5	21.5	114	1 S206_HUMAN	P80162 homo sapien
36	76.5	21.2	71	1 S206_RABIT	P30782 coryctolagus
37	76.5	21.2	112	1 S206_BOVIN	P80221 bos taurus
38	76.5	21.2	119	1 S207_PIG	P43030 sus scrofa
39	76	21.1	96	1 E07A_CAVPO	P80325 cavia porce
40	75.5	20.9	97	1 E07A_RAT	P97545 rattus norv
41	75.5	20.9	107	1 M12B_HUMAN	P19876 homo sapien
42	73.5	20.4	92	1 SY04_RABIT	P46632 coryctolagus
43	73.5	20.4	100	1 MIP2_RAT	P30348 rattus norv
44	73.5	20.4	103	1 EMP1_CHICK	P08317 gallus gall
45	73.5	20.4	132	1 S205_MOUSE	P50228 mus musculu

ALIGNMENTS

RESULT 1

ID SDF1_FELCA STANDARD: PRT: 93 AA.

AC 062657; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).

GN SDF1

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_Taxid:9685;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;

RA MEDLINE=98450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Cai J.S., Sato E., Kohmoto M., Mikami T.;

Molecular cloning and sequencing of feline stromal cell-derived factor-1 alpha and beta.;

RT Eur. J. Immunogenet. 25:303-305(1998).

RL -I- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT NOT NEUTROPHILS.

CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AB011966; BAA28602.1; -

CC HSSP: P48061; ISDF.

CC InterPro: IPR001089; CXC_chimkine_sm11.

CC InterPro: IPR001811; Chemokine_IL8.

CC Pfam: PF00048; IL8; 1.

CC SMART: SM00199; SCY; 1.

CC PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.

CC CYTOKINE: Chemotaxis; Growth factor; Signal; Alternative splicing.

CC SIGNAL 1

FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.

FT DISULFID 32 55 BY SIMILARITY.

FT FT 32 71 MISSING (IN ISOFORM ALPHA).

FT VARSPLIC 90 93 MISSING (IN ISOFORM ALPHA).

FT FT 93 AA; 10581 MW; 44FC763711E9BE37 CRC64;

SO SEQUENCE

Query Match 95.3%; Score 344; DB 1; Length 93;

Best local Similarity 97.0%; Pred. No. 2e-35;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RA Weinstein I.B.:
 RT "Molecular cloning of TPAP1, a gene whose expression is repressed by
 RT the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
 RL Exp. Cell Res. 215:284-293(1994).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AKR/J;
 RA Nomura M., Nakata Y., Uzuwa A., Nose M., Akashi M., Suzuki G.:
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 CC NOT NEUTROPHILS.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
 CC PRECURSOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
 CC STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE INTERCINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D21072; BAA04648.1; -
 DR EMBL: L12029; AAA40100.1; -
 DR EMBL: L12030; AAA40101.1; -
 DR EMBL: S74318; AAB32650.1; -
 DR EMBL: D43804; BAA07862.1; -
 DR EMBL: D43805; BAA07863.1; -
 DR PIR: A53497; A53497.
 DR HSSP: P48061; 1SDP.
 DR MGD: MGI:103556; Sdfl.
 DR InterPro: IPR001089; CXC_cmkine_sm11.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 DR KMW Cycleline; Chemotaxis; Growth factor; Signal; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.
 FT DISULFID 30 55
 FT DISULFID 32 71 BY SIMILARITY.
 FT VARSPLIC 89 89 K -> KRLLK (IN ISOFORM BETA).
 SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;
 Query Match
 Best Local Similarity 95.0%; Score 343; DB 1; Length 89;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 KGVSLSTYPCPCRFESFHVARNVKKILINTPCALQIVARLKNNNROYCIDPKLWIOE 60
 Db 22 KPVSLSTYPCPCRFESFHVARNVKKILINTPCALQIVARLKNNNROYCIDPKLWIOE 81
 Oy 61 YLEKALN 67
 Db 82 YLEKALN 88
 RESULT 4
 IL8_CANVO
 ID IL8_CANVO STANDARD: PRT: 101 AA.
 AC P49113;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein
 DE 1) (NAP-1).
 GN IL8.
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathia; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=94065176; PubMed=7504015;
 RA Yoshimura T., Johnson D.G.:
 RT "CDNA cloning and expression of guinea pig neutrophil attractant
 RT protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";
 RL J. Immunol. 151:6225-6236(1993).
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L04986; AAB37049.1; -
 DR HSSP: P10145; 2IL8.
 DR InterPro: IPR001089; CXC_cmkine_sm11.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR KMW Cycleline; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 101 INTERLEUKIN-8.
 FT DISULFID 34 61 BY SIMILARITY.
 FT DISULFID 36 77 BY SIMILARITY.
 SQ SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;
 Query Match
 Best Local Similarity 27.1%; Score 98; DB 1; Length 101;
 Matches 21; Conservative 17; Mismatches 17; Indels 6; Gaps 4;
 Oy 11 CRFFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNNROYCIDPKLWIOEYLEKA 65
 Db 34 CQCKIKHTTPHPKPFKELKVIESGRCANSEIIVKL-SDNRQLCDLPKKWQDVVSMF 92
 Oy 66 L 66
 Db 93 L 93
 RESULT 5
 IL8_CANFA
 ID IL8_CANFA STANDARD: PRT: 101 AA.
 AC P41324;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN IL8.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010328; PubMed=7916715;
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.:
 RT "Cloning of a canine gene homologous to the human

```

RT Interleukin-8-encoding gene.;
RL gene 131:305-306(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node;
RX MEDLINE=95127913; PubMed=7827282;
RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,
RA Goltzuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshinara K.,
RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;
RT "Molecular cloning and expression of canine interleukin 8 cDNA.";
RL Cytokine 6:455-461(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Montgrel; TISSUE=Jugular vein;
RX MEDLINE=95114148; PubMed=7814650;
RA Kukielka G.L., Smith W.C., Larosa G.J., Manning A.M.,
RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,
RA Michael L.H., Rot A., Entman M.L.;
RT "Interleukin-8 gene induction in the myocardium after ischemia and
RT reperfusion in vivo.";
RL J. Clin. Invest. 95:89-103(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle;
RX MEDLINE=97230298; PubMed=9119462;
RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;
RT "Borrelia burgdorferi migrates into joint capsules and causes an up-
RT regulation of interleukin-8 in synovial membranes of dogs
RT experimentally infected with ticks.";
RL Infect. Immun. 65:1273-1285(1997).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D28772; BAA05961.1; -
DR EMBL: D14285; BAA03246.1; -
DR EMBL: U10308; AAC48434.1; -
DR EMBL: AF048717; AAC05134.1; -
DR HSSP: P10145; 1IKM
DR InterPro: IPR001089; CXK_chmkin-smll
DR InterPro: IPR001811; Chemokine_IL8
DR Pfam: PF00048; IL8; 1
DR PRINTS: PR00437; SMALLCYTCKCX
DR SMART: SM00199; SCY; 1
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT CHAIN 1 22 BY SIMILARITY.
FT STAGN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;
Query Match 26.0%; Score 94; DB 1; Length 101;
Best Local Similarity 34.7%; Pred. No. 9.6e-05;
Matches 25; Conservative 15; Mismatches 20; Indels 12; Gaps 5;
OY 3 VSLSYPCPCRFRESHVAVKAVKHLKILNT---PNCALQIVARLKNNNOVCIDPKLKW 57
DB 28 VSSLRLCQC--IKTHSPFHPKPKYIKELRLVIDSGPHENSEIIVLFGNG--EVCIDPKKXW 84

```

```

OY 58 IOE----YLEKA 65
DB 85 VQKVVOIFLEKKA 96
RESULT 6
SY05_MOUSE STANDARD; PRT; 91 AA.
ID SY05_MOUSE
AC P30882;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CC15) (T-cell specific RANTES
DE protein) (Sis-delta) (Murantes).
GN SCY45.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92277990; PubMed=1375672;
RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
RA Krensky A.M., Neilson E.G.;
RT "Isolation and characterization of cDNA from renal tubular epithelium
RT encoding murine Rantes.";
RL Kidney Int. 41:220-225(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92289805; PubMed=1376260;
RA Schall T.J., Simpson N.J., Mak J.Y.;
RT "Molecular cloning and expression of the murine RANTES cytokine;
RT structural and functional conservation between mouse and man.";
RL Eur. J. Immunol. 22:1477-1481(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RX MEDLINE=94132613; PubMed=7507961;
RA Danhoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
RT "Cloning, genomic organization and chromosomal localization of the
RT Scy45 gene encoding the murine chemokine RANTES.";
RL J. Immunol. 152:1182-1189(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94217689; PubMed=7513046;
RA Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,
RA Paznekas W.A.;
RT "Definition of a lipopolysaccharide-responsive element in the 5'-
RT flanking regions of Murantes and crg-2.";
RL Mol. Cell. Biol. 14:2914-2925(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ.B10.S/J, NOD/LTJ, and SJL/J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RT Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M77747; AAA40029.1; -

```



```

RESULT 9
SY02_CAVPO
ID SY02_CAVPO STANDARD: PRT: 120 AA.
AC 008782;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCYA2 OR MCP1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=; TISSUE=Spleen;
RX MEDLINE=93267104; PubMed=8496603;
RA Yoshimura T.;
RT "cDNA cloning of guinea pig monocyte chemoattractant protein-1 and
expression of the recombinant protein.";
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sdb.ch/announce/
or send an email to license@sdb.ch).
-----
DR EMBL: L04985; AAA37047.1; .
DR HSSP: P80098; 1B00.
DR InterPro: IPR000827; CC-Chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 120 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 120 AA: 13741 MW: 5905596851CFIC54 CRC64;
Query Match 25.2%; Score 91; DB 1; Length 120;
Best Local Similarity 29.8%; Pred. No. 0.00027;
Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;
OY 8 PCPCFFESHVARANKYKILNTPGALQIYARLKNNNROYCIDPKLKWIDYLEK 64
DB 31 PTCYTFNKQIPLKRKYGERITSRCPQEAIVFRTLKNKVCADPTQWVDYIAK 87
PRT: 99 AA.
IL8_HUMAN
ID IL8_HUMAN STANDARD: PRT: 99 AA.
AC P10145; Q9C077; Q96R66;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil
chemotactic factor) (MDCNF) (T-cell chemotactic factor) (Neutrophil-

```

```

activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-
activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating
factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emoctrakin).
GN IL8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258376; PubMed=3260265;
RA Matsushima K., Morishita K., Yoshimura T., Lavu S., Kobayashi Y.,
RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;
RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic
factor (MDCNF) and the induction of MDCNF mRNA by interleukin 1 and
tumor necrosis factor.";
RL J. Exp. Med. 167:1883-1893(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87224164; PubMed=2953813;
RA Schmid J., Weissmann C.;
RT "Induction of mRNA for a serine protease and a
beta-thromboglobulin-like protein in mitogen-stimulated human
leukocytes.";
RL J. Immunol. 139:250-256(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89313739; PubMed=2664463;
RA Kowalski J., Denhardt D.T.;
RT "Regulation of the mRNA for monocyte-derived neutrophil-activating
peptide in differentiating HL60 promyelocytes.";
RL Mol. Cell. Biol. 9:1946-1957(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89309626; PubMed=2663993;
RA Mukaida N., Shitoo M., Matsushima K.;
RT "Genomic structure of the human monocyte-derived neutrophil
chemotactic factor IL-8.";
RL J. Immunol. 143:1366-1371(1989).
RN [5]
RP SEQUENCE FROM N.A.
RA Ishikawa J.;
RL Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Jang J.S., Kim B.E.;
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN [8]
RP SEQUENCE OF 23-46.
RX MEDLINE=89246368; PubMed=2655583;
RA Golds E.E., Mason P., Nyirkos P.;
RT "Inflammatory cytokines induce synthesis and secretion of gro protein
and a neutrophil chemotactic factor but not beta 2-microglobulin in
human synovial cells and fibroblasts.";
RL Biochem. J. 259:585-588(1989).
RN [9]
RP SEQUENCE OF 23-54.
RX MEDLINE=89279141; PubMed=2659722;
RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,
RA Mizuno S.;
RT "Purification and partial primary sequence of a chemotactic protein
for polymorphonuclear leukocytes derived from human lung giant cell
carcinoma Lu65C cells.";
RL J. Exp. Med. 169:1895-1901(1989).
RN [10]
RP SEQUENCE OF 28-99.
RX MEDLINE=88162914; PubMed=3279957;
RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;

```

RT "structure determination of a human lymphocyte derived neutrophil
RT activating peptide (LYNAP).";
RL Biochem. Biophys. Res. Commun. 151:883-890(1988).
RN [11]
RP SEQUENCE OF 28-59.
RX MEDLINE=88106502; PubMed=3322281;
RA Walz A., Peyerl P., Aschner H., Baggiolini M.;
RT "Purification and amino acid sequencing of NAF, a novel neutrophil-
RL activating factor produced by monocytes.";
RL Biochem. Biophys. Res. Commun. 149:755-761(1987).
RN [12]
RP SEQUENCE OF 28-69.
RX MEDLINE=88097462; PubMed=3480540;
RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,
RT Oppenheim J.J., Leonard E.J.;
RT "Purification of a human monocyte-derived neutrophil chemotactic
RT factor that has peptide sequence similarity to other host defense
RT cytokines";
RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).
RN [13]
RP N-TERMINAL FORMS.
RX MEDLINE=91006326; PubMed=2145175;
RA van Damme J., Rampart M., Coning R., Decock B., van Osselaer N.,
RT Williams J., Billiau A.;
RT "The neutrophil-activating proteins interleukin 8 and beta-
RT thromboglobulin: In vitro and in vivo comparison of NH2-terminally
RT processed forms.";
RL Eur. J. Immunol. 20:2113-2118(1990).
RN [14]
RP N-TERMINAL FORMS.
RX MEDLINE=89231715; PubMed=2532801;
RA van Damme J., Van Beeumen J., Conings R., Decock B., Billiau A.;
RT "Purification of granulocyte chemotactic peptide/interleukin-8
RT reveals N-terminal sequence heterogeneity similar to that of
RT beta-thromboglobulin.";
RL Eur. J. Biochem. 181:337-344(1989).
RN [15]
RP SYNTHESIS OF 28-99.
RX MEDLINE=91175767; PubMed=2007144;
RA Alberts-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,
RT Abersold R.;
RL "Chemical synthesis, purification, and characterization of two
RT inflammatory proteins, neutrophil activating peptide 1
RT (interleukin-8) and neutrophil activating peptide.";
RL Biochemistry 30:3128-3135(1991).
RN [16]
RP REVIEW.
RX MEDLINE=92347562; PubMed=1639201;
RA Baggiolini M., Clark-Lewis I.;
RT "Interleukin-8, a chemotactic and inflammatory cytokine.";
RL FEBS Lett. 307:97-101(1992).
RN [17]
RP STRUCTURE BY NMR.
RX MEDLINE=90234679; PubMed=2184886;
RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;
RT "Three-dimensional structure of interleukin 8 in solution.";
RL Biochemistry 29:1689-1696(1990).
RN [18]
RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.
RX MEDLINE=9118123; PubMed=10368283;
RA Skelton N.J., Quan C., Reilly D., Lowman H.;
RT "Structure of a CXCR chemokine-receptor fragment in complex with
RT interleukin-8";
RL Structure 7:157-168(1999).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=90216714; PubMed=2182630;
RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,
RT Wlodawer A., Weber I.T.;
RT "Crystallization of human interleukin-8. A protein chemotactic for
RT neutrophils and T-lymphocytes.";
RL J. Biol. Chem. 265:6851-6853(1990).
RN [20]

[illegible]

RX MEDLINE=88285659; PubMed=2456327;
 RA Schall T.J., Jonsgstra J., Dyer B.J., Jorgensen J., Clayberger C.,
 RA Davis M.M., Kremsky A.M.;
 RT "A human T cell-specific molecule is a member of a new gene family.";
 RL J. Immunol. 141:1018-1025(1988).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Jang J.S., Kim B.E.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99228475; PubMed=10213461;
 RA Nomiyama H., Fukuda S., Ito M., Tanase S., Miura R., Yoshie O.;
 RT "Organization of the chemokine gene cluster on human chromosome
 RT 17q11.2 containing the genes for CC chemokine MIP-1, HCC-2, LEC, and
 RT RANTES.";
 RL J. Interferon Cytokine Res. 19:227-234(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zeng Q.P., Yang R.Y., Fu L.C.;
 RT "The complete sequence of human beta-chemokine RANTES mRNA.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.
 RX MEDLINE=96106406; PubMed=8525373;
 RA Cocchi F., Devico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
 RA Lusso P.;
 RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major
 RT HIV-suppressive factors produced by CD8+ T cells.";
 RL Science 270:1811-1815(1995).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95352612; PubMed=7542919;
 RA Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C.;
 RT "The three-dimensional solution structure of RANTES.";
 RL Biochemistry 34:9307-9314(1995).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95244456; PubMed=7537088;
 RA Skelton N.J., Aspinas F., Ogez J., Schall T.J.;
 RT "Proton NMR assignments and solution conformation of RANTES, a
 RT chemokine of the C-C type.";
 RL Biochemistry 34:5329-5342(1995).
 RN [9]
 RN SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=9911238; PubMed=9889151;
 RA Wilken J., Hoover D., Thompson D.A., Barlow P.N., Mesparion H.,
 RA Picard L., Wlodawer A., Lubkowski J., Kent S.B.;
 RT "Total chemical synthesis and high-resolution crystal structure of
 RT the potent anti-HIV protein AOP-RANTES.";
 RL Chem. Biol. 6:43-51(1999).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RA Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C.,
 RA Lubkowski J.;
 RT "The crystal structure of Met-RANTES: comparison with native RANTES
 RT and AOP-RANTES.";
 RL Protein Pept. Lett. 7:73-82(2000).
 CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
 CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
 CC BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND
 CC CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T
 CC CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT
 CC INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN
 CC IMMUNODEFICIENCY VIRUS (SIV).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
 CC -I- INDUCTION: BY MITOGENS.

CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL: M21121; AAA36725.1; -
 DR EMBL: AF043341; AAC03541.1; -
 DR EMBL: AF088219; AAC6331.1; -
 DR EMBL: AF266753; AAF73070.1; -
 DR EMBL: BC008600; AAH08600.1; -
 DR PIR: A28815; A28815.
 DR PDB: 1HRJ; 14-OCT-96.
 DR PDB: 1RTN; 03-JUN-95.
 DR PDB: 1RTO; 03-JUN-95.
 DR PDB: 1B3A; 23-APR-99.
 DR PDB: 1EQT; 19-APR-00.
 DR Genew; HGNC:10632; SCYA5.
 DR MIM; 187011; -
 DR InterPro; IPR000827; CC_chemkine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;
 KW 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
 FT DISULFID 33 57
 FT DISULFID 34 73
 FT CONFLICT 7 7
 FT CONFLICT 14 14 A -> R (IN REF. 1 AND 4).
 FT SEQUENCE 91 AA; 9990 MW; F80BFAF9A87C620P CRC64;
 SQ
 Query Match 24.5%; Score 88.5; DB 1; Length 91;
 Best Local Similarity 30.9%; Pred No. 0.00041;
 Matches 17; Conservative 12; Mismatches 25; Indels 1; Gaps 1;
 QY 8 PCPCRFESHVARANVHKILNTPNCALQIVARLNKNNRQVCIDPRKLVIOEYL 62
 Db 32 PCGFATVATRLPRAHIKEY-FYTSGRCSNPAVVFVTRKNRQVCANPEKKWVREYI 85
 ID SY05_CAVPO STANDARD; PRT; 91 AA.
 AC P97272; 009076;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small Inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
 DE protein) (SIS-delta).
 GN SCYA5.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dunkin-Hartley;
 RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B.,
 RA Wells T.N.C., White A.M., Westwick J., Watson M.L.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A.,
 RA Yamaguchi K., Kanazawa M.;


```
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHEMOTACTICANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U77037; AAC53293.1; -.
CC EMBL: AB002662; BAAL9604.1; -.
CC HSSP: P13501; 1RTN.
CC InterPro: IPR000827; CC_chemokine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: SM00199; SCY; 1.
CC PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC Cyclokin: Chemotaxis; T-cell; Signal; Inflammatory response.
CC SIGNAL 1 23
CC CHAIN 1 23
CC DISULFID 33 57
CC DISULFID 34 73
CC SEQUENCE 91 AA: 10088 MW: 766A31B751237DB9 CRC64:

Query Match 24.2%; Score 87.5; DB 1: Length 91;
Best Local Similarity 33.9%; Pred. No. 0.00054;
Matches 19; Conservative 14; Mismatches 18; Indels 5; Gaps 3;

Oy 10 PCRFESHVARANVK-HLK--ILNTPNCALQIVARLKNNNRQVCIDPKLWIOEYL 62
Db 32 PCCF--AVISRALPRTHTKEYFYTSSKSNLAVFVETKRNQVCANPEKKWREYI 85

RESULT 13
IL8_MACMU STANDARD: PRT: 101 AA.
ID IL8_MACMU
AC P51495:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=7628861;
RA Minerly J.C., Baganoft M.P., Depeeler C.L., Keller B.T.,
RA Rapp S.R., Widomski D.L., Fretland D.J., Bolanowski M.A.;
RT "Identification and characterization of rhesus macaque
RT Interleukin-8.";
RL Inflammation 19:313-331(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
```

```
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U19849; AAA86711.1; -.
CC EMBL: U19851; AAA86713.1; -.
CC EMBL: S78555; AAA80141.2; -.
CC HSSP: P10145; 2IL8.
CC InterPro: IPR001089; CXCL_chemokine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC PRINTS: PR00437; SMALLCYTOKXC.
CC SMART: SM00199; SCY; 1.
CC PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
CC Cyclokin: Chemotaxis; Inflammatory response; Signal.
CC SIGNAL 1 22
CC CHAIN 1 22
CC DISULFID 23 101
CC DISULFID 34 61
CC DISULFID 36 77
CC SEQUENCE 101 AA: 11320 MW: 42BCF9C97C84B5F9 CRC64:

Query Match 24.2%; Score 87.5; DB 1: Length 101;
Best Local Similarity 36.4%; Pred. No. 0.0006;
Matches 16; Conservative 16; Mismatches 9; Indels 3; Gaps 3;

Oy 23 VKHLKI LNT- PNCA- LQIVARLKNNNRQVCIDPKLWIOEYLEK 64
Db 49 IKELRVIESGPHICANTEIIVKL-SDGRELCIDPKPEWQRYVEK 91

RESULT 14
IL8_SHEEP STANDARD: PRT: 101 AA.
ID IL8_SHEEP
AC P36925:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95121931; PubMed=7821808;
RA Legasteleis I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RT "Sequencing of the ovine Interleukin-8-encoding cDNA using the
RT polymerase chain reaction.";
RL Gene 150:367-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137691; PubMed=7835984;
RA Seow H.F., Yoshimura T., Wood P.R., Golditz I.G.;
RT "Cloning, sequencing, expression and inflammatory activity in skin of
RT ovine interleukin-8.";
RL Immunol. Cell Biol. 72:398-405(1994).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
```

```

CC -1 SUBUNIT: HOMODIMER.
CC -1 SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X78306; CAAS5115.1; -
DR EMBL: S74436; AAB33241.1; -
DR PIR: S42496; S42496.
DR HSSP: P10145; 1IKM.
DR InterPro: IPR001089; CXCL_chmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXCL.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR CYTOKINE: Chemotaxis; Inflammatory response; signal.
FT SIGNAL: 1 22 BY SIMILARITY.
FT CHAIN: 23 101 INTERLEUKIN-8.
FT DISULFID: 34 61 BY SIMILARITY.
FT DISULFID: 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11292 MW; 40E8418B57C56A5B CRC64;

```

Query Match 24.1%; Score 87; DB 1; Length 101;

Best Local Similarity 29.5%; Pred. No. 0.00069;

Matches 18; Conservative 20; Mismatches 17; Indels 6; Gaps 4;

```

QY 11 CPREFESHVARAN--VKHLKILNT-PNCA-LOIVARLKNRRVCIDPKLWIOEYLEKA 65
   1:  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 34 CQCIKHSHPHFHKFKIKELRVISGPHCENSELIVKL-TNGKEVCLDPKEXKQVKYQAR 92

```

```

QY 66 L 66
Db 93 L 93

```

```

RESULT 15
GRO_MOUSE STANDARD: PRT; 96 AA.
AC P12850;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth regulated protein precursor (CXCL1) (platelet-derived growth
DE factor-inducible protein KC) (Secretory protein N51).
GN SCY1 OR GRO1 OR GRO OR MGS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89139485; PubMed=2917992;
RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
RT "The platelet-derived growth factor-inducible KC gene encodes a
RT secretory protein related to platelet alpha-granule proteins.";
RL J. Biol. Chem. 264:4133-4137(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89078502; PubMed=2909392;
RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
RT "Cloning and sequence of a secretory protein induced by growth
RT factors in mouse fibroblasts.";
RL Exp. Cell Res. 180:266-275(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;

```

```

RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,
RA Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96016008; PubMed=7561058;
RA Ohmori Y., Fukumoto S., Hamilton T.A.;
RT "Two structurally distinct kappa B sequence motifs cooperatively
RT control LPS-induced KC gene transcription in mouse macrophages.";
RL J. Immunol. 155:3593-3600(1995).
CC -1 FUNCTION: HAS CHEMOKINE ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
CC -1 INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG. BY
CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04596; AAA40131.1; -
DR EMBL: U20634; AAB03376.1; -
DR EMBL: U20527; AAB03376.1; JOINED.
DR EMBL: S79767; -, NOT_ANNOTATED_CDS.
DR PIR: A32954; A32954.
DR PIR: JH0081; JH0081.
DR HSSP: P19875; 1ONK.
DR MGD: MGI:108068; Gro1.
DR InterPro: IPR001089; CXCL_chmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXCL.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR CYTOKINE: Growth factor; Inflammatory response; signal.
FT SIGNAL: 1 24 PROBABLE.
FT CHAIN: 25 96 GROWTH REGULATED PROTEIN.
FT DISULFID: 33 59 BY SIMILARITY.
FT DISULFID: 35 75 BY SIMILARITY.
SQ SEQUENCE 96 AA; 10254 MW; 4A52B5EC38B45C2 CRC64;

```

Query Match 24.0%; Score 86.5; DB 1; Length 96;

Best Local Similarity 31.7%; Pred. No. 0.00076;

Matches 19; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

```

QY 9 CPREFESHVARANVKHLKIL-NTPNCA-LOIVARLKNRRVCIDPKLWIOEYLEKAL 66
   1:  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 33 CQCIKHSHPHFHKFKIKELRVISGPHCENSELIVKL-TNGKEVCLDPKEXKQVKYQAR 91

```

Search completed: January 23, 2003, 15:34:20

Job time : 7 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 ; Search time 22.6 Seconds
(without alignments)
610.848 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361
Sequence: 1 KGVSLSTPCPCRFESHVAR.....QVCIDPKMKIQLYELKALN 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.3	92	4	Q9H554
2	336	93.1	89	11	Q9QZD1
3	278	77.0	94	13	Q8UJ39
4	98.5	27.3	91	11	Q912L1
5	87.5	24.2	363	13	Q90ZT0
6	87.5	24.2	1096	13	Q90ZT1
7	87	24.1	98	13	Q8QGV8
8	87	24.1	109	13	Q90Y59
9	84.5	23.4	79	4	Q95689
10	84.5	23.4	883	13	Q91493
11	83.5	22.9	134	12	Q9YV49
12	82.5	22.9	142	12	Q91B07
13	82.5	22.9	601	13	Q73928
14	80	22.2	148	11	Q9QYD7
15	80	22.2	203	12	Q67634
16	78.5	21.7	97	11	Q9Z318

17	78	21.6	104	13	Q73912	073912 gallus gall
18	76	21.1	106	11	Q9Z292	09Z292 cricetus
19	75.5	20.9	91	13	Q8Q556	08Q556 gallus gall
20	75	20.8	97	13	Q8Q5P5	08Q5P5 cyprinus ca
21	74.5	20.6	101	13	Q93442	093442 lampetra fl
22	74.5	20.6	108	6	Q28724	Q28724 oryctolagus
23	72.5	20.1	97	6	Q9TTS6	Q9TTS6 bos taurus
24	72	19.9	97	13	Q9RMO2	Q9RMO2 oncorhynch
25	71.5	19.8	92	6	Q8SQ40	Q8SQ40 felis silve
26	71.5	19.8	100	11	Q912K9	Q912K9 sigmodon hl
27	71.5	19.8	101	11	Q91264	Q91264 gallus gall
28	71	19.7	89	13	Q918E0	Q918E0 gallus gall
29	71	19.7	95	12	Q98158	Q98158 kaposi's sa
30	71	19.7	102	6	Q95M77	Q95M77 ovis aries
31	70	19.4	91	13	Q8Q557	Q8Q557 gallus gall
32	70	19.4	96	13	Q90825	Q90825 gallus gall
33	70	19.4	101	13	Q8QW91	Q8QW91 triakis scy
34	69.5	19.3	100	6	Q9TTO4	Q9TTO4 equus caball
35	69.5	19.3	150	11	Q9QW66	Q9QW66 mus sp. dys
36	69.5	19.3	258	11	Q9D6J7	Q9D6J7 mus musculu
37	69.5	19.3	622	4	Q02295	Q02295 homo sapien
38	69.5	19.3	3685	4	Q14205	Q14205 homo sapien
39	69	19.1	80	4	Q14745	Q14745 homo sapien
40	69	19.1	93	4	Q96168	Q96168 homo sapien
41	69	19.1	100	6	Q95MD5	Q95MD5 bos taurus
42	69	19.1	395	11	Q91V44	Q91V44 mus musculu
43	68.5	19.0	126	11	Q99J60	Q99J60 mus musculu
44	68	18.8	81	11	Q9QZ01	Q9QZ01 rattus norv
45	68	18.8	92	11	Q912H5	Q912H5 rattus norv

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	92 AA.
ID Q9H554	Q9H554		
AC Q9H554:	Q9H554:		
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)			
DE (Fragment).			
GN SDPL			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Bird C.;			
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.			
DR EMBL; AL137026; CAC10202.1; .			
DR HSSP; P48061; ISDF.			
DR InterPro; IPR001811; Chemokine_IL8.			
DR Pfam; PF00048; IIR.1.			
DR SMART; SM00199; SCY.1.			
FT NON_TER			
FT SEQUENCE 92 AA; 10510 MW; AEF0C402B44E8D20 CRC64;			
Query Match	95.3%	Score 344;	DB 4; Length 92;
Best Local Similarity	97.0%;	Pred. No. 1.4e-35;	
Matches 65;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY 1 KGVSLSTPCPCRFESHVARAVKHLKTLTPNCALQIVARLKNRRVQCIDPKLKWIOE 60			
DB 22 KPVSLSTPCPCRFESHVARAVKHLKTLTPNCALQIVARLKNRRVQCIDPKLKWIOE 81			
QY 61 YLEKALN 67			
DB 82 YLEKALN 88			

```

RESULT 2
Q90ZD1 PRELIMINARY: PRT: 89 AA.
AC Q90ZD1:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "CDNA cloning of rat Stromal cell-derived factor-1 alpha (SDF-1
RT alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillarisetti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
RT alpha chemokine, Stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189724; AAF01066.1; -.
DR EMBL: AF209976; AAG43506.1; -.
DR HSP: P48061; ISDF.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
SQ SEQUENCE 89 AA: 9977 MW: D86977626A2E35FA CRC64;

```

```

Query Match 93.1%; Score 336; DB 11; Length 89;
Best Local Similarity 94.0%; Pred. No. 1.4e-34;
Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSPCCRFESHVARANKHLKILNTPGALQIYARLKNRRQVCIDPKLKWIOE 60
DB 22 KPVSLYRCPCRFESHVARANKHLKILNTPGALQIYARLKNRRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

```

```

RESULT 3
Q80UJ9 PRELIMINARY: PRT: 94 AA.
AC Q80UJ9:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis Stromal-derived factor 1: conservation of structure
RT and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278857; CAC82196.1; -.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
KW Signal.

```

```

FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.
SQ SEQUENCE 94 AA: 10701 MW: 8C8325D152F326E7 CRC64;

```

```

Query Match 77.0%; Score 278; DB 13; Length 94;
Best Local Similarity 73.1%; Pred. No. 2.7e-27;
Matches 49; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSPCCRFESHVARANKHLKILNTPGALQIYARLKNRRQVCIDPKLKWIOE 60
DB 22 KPVSLYRCPCRFESHVARANKHLKILNTPGALQIYARLKNRRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

```

```

RESULT 4
Q91ZL1 PRELIMINARY: PRT: 91 AA.
AC Q91ZL1:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE RANPES Chemokine.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF421391; AAL16932.1; -.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
SQ SEQUENCE 91 AA: 10082 MW: D0D6EAE8E4242FF CRC64;

```

```

Query Match 27.3%; Score 98.5; DB 11; Length 91;
Best Local Similarity 36.4%; Pred. No. 8.4e-05;
Matches 20; Conservative 10; Mismatches 24; Indels 1; Gaps 1;

```

```

QY 8 PCPCRFESHVARANKHLKILNTPGALQIYARLKNRRQVCIDPKLKWIOEYL 62
DB 32 PCCEAYLSAVLPRAHKEY-FYTSSKCSNPAVVFYTRRRQVCANPKKRWQETI 85

```

```

RESULT 5
Q90ZT0 PRELIMINARY: PRT: 363 AA.
AC Q90ZT0:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin variant Dp71 (Fragment).
GN DMD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184125; PubMed=11287201;
RA Bolanos-Jimenez F., Borda A., Behra M., Strahle U., Sahel J.,
RA Rendon A.;
RT "Dystrophin and Dp71, two products of the DMD gene, show a different
RT pattern of expression during embryonic development in zebrafish.";
RL Mech. Dev. 102:239-241(2001).

```



```

CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FORESKIN;
RA Bartels J.H., Schluter C., Richter E., Noso N., Christophers E.,
RA Schroeder J.M.;
RT "Expression of a MCP-4 like novel CC-chemokine in human dermal
RL fibroblasts: molecular cloning and RT-PCR analysis.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z77650; CAB0111.1; -.
DR HSSP: P51671; IEOT.
DR InterPro: IPR000827; CC_chemkine.sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
FT NON TER 1
SQ SEQUENCE 79 AA; 8987 MW; 4FCF42983D6C352 CRC64;

Query Match 23.4%; Score 84.5; DB 4; Length 79;
Best Local Similarity 30.2%; Pred. No. 0.0041;
Matches 19; Conservative 15; Mismatches 24; Indels 5; Gaps 3;

Oy 4 SLSYCPQCF-FESHVARNVKHK--LINTNCALQIYARLKNNRQVCIDPKIKWQE 60
   :| | | | | : : : | | | | | : : : | | | | |
Db 11 ALNVSTCCFFPS--KKISLRKLSYVITTSRCPQKAVIFPTKLGLKICADPKERKWON 68
   :| | | | | : : : | | | | | : : : | | | | |

Oy 61 YLE 63
   | :
Db 69 YMK 71

RESULT 10
O91493 PRELIMINARY; PRT; 883 AA.
AC O91493:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN DYSTROPHIN.
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogadidae; Batoidae;
OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
OX NCBI_TaxID=7787;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92064638; Pubmed=1720119;
RA Yeodon J.E., Lin H., Dyer S.M., Burden S.J.;
RT "Dystrophin is a component of the subsynaptic membrane.";
RL J. Cell Biol. 115:1069-1076(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92291902; Pubmed=1818109;
RA Ravin A.J., Dyer S.M., Yeodon J.E., Burden S.J.;
RT "Multiple dystrophin isoforms are associated with the postsynaptic
RL membrane of Torpedo electric organ.";
RL J. Physiol. (Paris) 85:131-133(1991).
DR EMBL: M37645; AAC38002.1; -.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR001202; WW_Rsp5_WMP.
DR InterPro: IPR000433; ZnF_ZZ.
DR Pfam: PF00397; WW; 1.
DR Pfam: PF00569; zz; 1.
DR SMART: SM00150; SPEC; 2.
DR SMART: SM00456; WW; 1.
DR SMART: SM00291; ZnF_ZZ; 1.
DR PROSITE: PS01159; WW_DOMAIN_1; 1.
DR PROSITE: PS00020; WW_DOMAIN_2; 1.
DR PROSITE: PS01357; zf_zz_1; UNKNOWN_1.

```

[illegible]

RP SEQUENCE FROM N.A.
RX MEDLINE=98167843; PubMed=9499411;

```

RESULT 15
Q67634 PRELIMINARY; 3 PRT; 203 AA.
AC Q67634;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Eco Q protein (Fragment).
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=96074534; PubMed=7491783;
RA Peng Q., Zeng M., Bhuiyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
RA Shirazi Y.;
RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
RT mapping to the BamHI-I2, BamHI-Q2, and BamHI-L fragments of the MDV
RT genome from lymphoblastoid cells transformed and persistently infected
RT with MDV.";
RL Virology 213:590-599(1995).
DR EMBL; U34966; AAC54629.1; -.
DR HSSP; P10889; 1MI2.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chemokine_smll.
DR InterPro; IPR004827; TF_DZIP.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
DR SMART; SM00338; BRL2; 1.
DR SMART; SM00199; SCV; 1.
FT NON_TER 1
SQ SEQUENCE 203 AA; 23132 MW; DE42F2A1C1A71C88 CRC64;

Query Match 22.2%; Score 80; DB 12; Length 203;
Best Local Similarity 28.4%; Pred. No. 0.04;
Matches 19; Conservative 13; Mismatches 17; Indels 18; Gaps 3;

QY 15 ESHVARANVKHLKILNTP-----NC-ALQIVARLKNRNQVCIDPKLKW 57
Db 95 ESLAVDKRCKVKVTRPTGLPIIADVIPPGLHGRRTTEIIPALK-KNRKVCVDPEAPW 153
QY 58 IOEYLEK 64
Db 154 VQOFIKK 160

```

Search completed: January 23, 2003, 15:36:21
Job time : 23.6 secs